

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 11:02:37 ; Search time 2765 Seconds
(without alignments)
10230.715 Million cell updates/sec

Title: US-09-992-430B-21
Perfect score: 972
Sequence: 1 atgttccaagatacaaaagtc.....ttgagcatctggagatcaat 972

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rnd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	23	2.4	151778	2	AC113646	AC113646 Rattus no
C 2	22	2.3	214265	2	AC099573	AC099573 Mus muscu
C 3	21	2.2	62004	2	AC114589	AC114589 Mus muscu
C 4	21	2.2	64969	9	AL355985	AL355985 Human DNA
C 5	21	2.2	150199	9	AC087568	AC087568 Pan trogl
C 6	21	2.2	169574	2	AC111597	AC111597 Rattus no
C 7	21	2.2	177066	9	AC091001	AC091001 Papio cyn
C 8	21	2.2	177893	9	AC005089	AC005089 Homo sapi
C 9	21	2.2	178228	2	AC128082	AC128082 Homo sapi
C 10	21	2.2	343550	1	AP003587	AP003587 Nostoc sp
C 11	20	2.1	188	9	HUMLDHX3	M24512 Homo sapien
C 12	20	2.1	811	9	AF401096	AF401096 Homo sapi
C 13	20	2.1	879	9	AF401095	AF401095 Homo sapi
C 14	20	2.1	1047	9	AF401097	AF401097 Homo sapi
C 15	20	2.1	1053	9	AF401094	AF401094 Homo sapi
C 16	20	2.1	1179	9	HUMLDHX	J02938 Human test
C 17	20	2.1	1204	9	AK058181	AK058181 Homo sapi
C 18	20	2.1	1215	4	VVU19868	U19868 Vulpes vulp
C 19	20	2.1	1243	6	I05686	I05686 Sequence 1
C 20	20	2.1	1250	9	BC019249	BC019249 Homo sapi
C 21	20	2.1	1254	9	HSU13680	U13680 Human lacta
C 22	20	2.1	2745	8	AF257777	AF257777 Vitis vin
C 23	20	2.1	13123	1	AE003872	AE003872 Xylella f
C 24	20	2.1	82625	2	AC097779	AC097779 Rattus no
C 25	20	2.1	87210	8	AB011485	AB011485 Arabidops
C 26	20	2.1	155085	2	AC025620	AC025620 Homo sapi
C 27	20	2.1	157402	2	AC013794	AC013794 Homo sapi
C 28	20	2.1	159998	2	AC074292	AC074292 Homo sapi
C 29	20	2.1	160930	9	AC010093	AC010093 Homo sapi
C 30	20	2.1	165633	2	AC026699	AC026699 Homo sapi
C 31	20	2.1	166973	9	AC084117	AC084117 Homo sapi
C 32	20	2.1	167916	2	AC094048	AC094048 Rattus no
C 33	20	2.1	174151	2	AC011182	AC011182 Homo sapi
C 34	20	2.1	176613	9	AC027708	AC027708 Homo sapi
C 35	20	2.1	177632	2	AC128367	AC128367 Rattus no
C 36	20	2.1	183263	2	AC127896	AC127896 Rattus no
C 37	20	2.1	186000	2	AC131014	AC131014 Rattus no
C 38	20	2.1	189893	9	AC011361	AC011361 Homo sapi
C 39	20	2.1	190352	2	AC097471	AC097471 Homo sapi
C 40	20	2.1	193657	2	AC105552	AC105552 Rattus no
C 41	20	2.1	196410	9	AC027544	AC027544 Homo sapi
C 42	20	2.1	202397	2	AC099232	AC099232 Rattus no
C 43	20	2.1	210533	2	AC099719	AC099719 Mus muscu
C 44	20	2.1	210841	2	AC121840	AC121840 Mus muscu
C 45	20	2.1	220101	2	AC121993	AC121993 Mus muscu
C 46	19	2.0	256	10	AB04820S05	AB047790 Mus muscu
C 47	19	2.0	1621	9	AK058192	AK058192 Homo sapi
C 48	19	2.0	1680	9	AY009108	AY009108 Homo sapi
C 49	19	2.0	1696	9	BC022034	BC022034 Homo sapi
C 50	19	2.0	2221	8	SPISF81A	M83940 Spinacia ol
C 51	19	2.0	2384	9	AK056891	AK056891 Homo sapi
C 52	19	2.0	2411	9	AK095799	AK095799 Homo sapi
C 53	19	2.0	2417	9	AK090755	AK090755 Homo sapi
C 54	19	2.0	2459	9	AK094806	AK094806 Homo sapi
C 55	19	2.0	2656	9	AK055499	AK055499 Homo sapi
C 56	19	2.0	2690	9	HSU07231	U07231 Homo sapien
C 57	19	2.0	2726	9	AK097055	AK097055 Homo sapi
C 58	19	2.0	4068	6	AX212239	AX212239 Sequence
C 59	19	2.0	4158	10	AB024336	AB024336 Mus muscu
C 60	19	2.0	21565	9	AL607068	AL607068 Human DNA
C 61	19	2.0	31312	9	AP000283	AP000283 Homo sapi
C 62	19	2.0	33140	6	AX067448	AX067448 Sequence
C 63	19	2.0	34968	3	U41534	U41534 Caenorhabdi
C 64	19	2.0	47403	6	AX059535	AX059535 Sequence
C 65	19	2.0	65970	9	AP000282	AP000282 Homo sapi

c 66	19	2.0	69513	2	AC131071	AC131071 Mus muscu
c 67	19	2.0	71272	2	AC103492	AC103492 Rattus no
c 68	19	2.0	73888	2	AC111426	AC111426 Rattus no
c 69	19	2.0	87286	2	AC014436	AC014436 Drosophill
c 70	19	2.0	91470	8	T4B21	AF118223 Arabidops
c 71	19	2.0	100000	9	AP000040	AF000040 Homo sapi
c 72	19	2.0	100000	9	AP000108	AP000108 Homo sapi
c 73	19	2.0	100000	9	AP000184	AP000184 Homo sapi
c 74	19	2.0	102196	9	AL590998	AL590998 Human DNA
c 75	19	2.0	109745	2	AC026447	AC026447 Homo sapi
c 76	19	2.0	110000	2	AC084053.2	Continuation (3 of
c 77	19	2.0	110000	2	AL359456.4	Continuation (5 of
c 78	19	2.0	110110	9	AC121337	AC121337 Homo sapi
c 79	19	2.0	111135	9	AL135933	AL135933 Human DNA
c 80	19	2.0	115915	9	AC105922	AC105922 Homo sapi
c 81	19	2.0	117743	2	AC109028	AC109028 Rattus no
c 82	19	2.0	119874	9	AL590096	AL590096 Human DNA
c 83	19	2.0	122467	9	AC123029	AC123029 Homo sapi
c 84	19	2.0	125108	9	AF030453	AF030453 Homo sapi
c 85	19	2.0	128532	2	AC128104	AC128104 Rattus no
c 86	19	2.0	135940	8	AC118603	AC118603 Oryza sat
c 87	19	2.0	137726	9	AC105919	AC105919 Homo sapi
c 88	19	2.0	140177	2	AC116245	AC116245 Rattus no
c 89	19	2.0	142504	2	AC129671	AC129671 Rattus no
c 90	19	2.0	143133	2	AC021655	AC021655 Homo sapi
c 91	19	2.0	148372	9	AC068388	AC068388 Homo sapi
c 92	19	2.0	150666	2	AC118817	AC118817 Rattus no
c 93	19	2.0	152185	2	AC012219	AC012219 Homo sapi
c 94	19	2.0	153619	2	AC130430	AC130430 Homo sapi
c 95	19	2.0	155182	2	AC023890	AC023890 Homo sapi
c 96	19	2.0	155221	9	AC016587	AC016587 Homo sapi
c 97	19	2.0	156264	2	AC102977	AC102977 Rattus no
c 98	19	2.0	159726	2	AC127949	AC127949 Rattus no
c 99	19	2.0	160380	9	AC112777	AC112777 Homo sapi
c 100	19	2.0	162354	9	AF260225	AF260225 Homo sapi
c 101	19	2.0	162876	3	AC098212	AC098212 Drosophill
c 102	19	2.0	164773	2	AC091543	AC091543 Felis cat
c 103	19	2.0	165933	8	AC131375	AC131375 Oryza sat
c 104	19	2.0	167439	2	AC130273	AC130273 Papio cyn
c 105	19	2.0	170914	3	AC010843	AC010843 Drosophill
c 106	19	2.0	171618	2	AC094532	AC094532 Rattus no
c 107	19	2.0	173067	9	AC083811	AC083811 Homo sapi
c 108	19	2.0	174033	2	AC021957	AC021957 Homo sapi
c 109	19	2.0	174084	2	AC084395	AC084395 Homo sapi
c 110	19	2.0	174311	9	AP002788	AP002788 Homo sapi
c 111	19	2.0	175034	2	AC130063	AC130063 Rattus no
c 112	19	2.0	176410	2	AC112712	AC112712 Homo sapi
c 113	19	2.0	176562	2	AC130272	AC130272 Papio cyn
c 114	19	2.0	179077	2	AC097075	AC097075 Rattus no
c 115	19	2.0	179323	2	AC011852	AC011852 Homo sapi
c 116	19	2.0	179591	9	AC093902	AC093902 Homo sapi
c 117	19	2.0	179693	2	AL691511	AL691511 Mus muscu
c 118	19	2.0	180069	9	AC007655	AC007655 Homo sapi
c 119	19	2.0	181191	9	AC117379	AC117379 Homo sapi
c 120	19	2.0	181700	2	AC128595	AC128595 Rattus no
c 121	19	2.0	181724	9	AC091983	AC091983 Homo sapi
c 122	19	2.0	181905	3	AC008211	AC008211 Drosophill
c 123	19	2.0	182087	2	AC055790	AC055790 Homo sapi
c 124	19	2.0	182087	2	AC055790	AC055790 Homo sapi
c 125	19	2.0	183784	2	AC101948	AC101948 Mus muscu
c 126	19	2.0	184001	9	AC104071	AC104071 Homo sapi
c 127	19	2.0	184692	2	AC094035	AC094035 Rattus no
c 128	19	2.0	185680	2	AC097378	AC097378 Homo sapi
c 129	19	2.0	185735	9	AC078785	AC078785 Homo sapi
c 130	19	2.0	185810	3	AC010995	AC010995 Drosophill
c 131	19	2.0	189534	2	AL354656	AL354656 Homo sapi
c 132	19	2.0	189999	9	AC092756	AC092756 Homo sapi
c 133	19	2.0	191137	2	AC124681	AC124681 Mus muscu
c 134	19	2.0	191275	2	AC015471	AC015471 Homo sapi
c 135	19	2.0	191440	2	AC095344	AC095344 Rattus no
c 136	19	2.0	192913	2	AC129214	AC129214 Mus muscu
c 137	19	2.0	193006	2	AC120599	AC120599 Rattus no
c 138	19	2.0	194872	10	AL590991	AL590991 Mouse DNA
c 139	19	2.0	196054	2	AC073388	AC073388 Mus muscu
c 140	19	2.0	198448	10	AC115118	AC115118 Mus muscu
c 141	19	2.0	200001	8	ATCHRIV13	AL61501 Arabidops
c 142	19	2.0	201805	10	AL606466	AL606466 Mouse DNA
c 143	19	2.0	201882	2	AC103345	AC103345 Rattus no
c 144	19	2.0	202972	10	AL663052	AL663052 Mouse DNA
c 145	19	2.0	203403	9	AC073130	AC073130 Homo sapi
c 146	19	2.0	205903	9	AP000901	AP000901 Homo sapi
c 147	19	2.0	207398	10	AL592462	AL592462 Mouse DNA
c 148	19	2.0	211902	3	AE003755	AE003755 Drosophill
c 149	19	2.0	215042	3	AC121594	AC121594 Mus muscu
c 150	19	2.0	219635	2	AC1390207	AC1390207 Homo sapi
c 151	19	2.0	238967	2	AC095377	AC095377 Rattus no
c 152	19	2.0	288763	2	AC124692	AC124692 Mus muscu
c 153	19	2.0	298839	3	AE003492	AE003492 Drosophill
c 154	19	2.0	305153	1	AP001520	AP001520 Bacillus
c 155	19	2.0	313573	3	CEY57G11C	Z99281 Caenorhabdi
c 156	19	2.0	316704	9	AF239258S3	AF239258 Homo sapi
c 157	19	2.0	337101	9	HSXKSRPXR	AL121578 Homo sapi
c 158	19	2.0	340000	1	AP001715	AP001715 Homo sapi
c 159	19	2.0	342800	1	AP003598	AP003598 Nostoc sp
c 160	18	1.9	803	9	AY077697	AY077697 Homo sapi
c 161	18	1.9	828	6	AX438187	AX438187 Sequence
c 162	18	1.9	1110	4	SSPQDMR	X16638 Pig p9d mRN
c 163	18	1.9	1268	10	CGU81045	U81045 Cricetus
c 164	18	1.9	1362	3	EDHXX2	Y11115 E. dispar mR
c 165	18	1.9	1371	3	EDHXX1	Y11114 E. dispar mR
c 166	18	1.9	1372	3	EDHXX1	X82197 E. histolyti
c 167	18	1.9	1376	3	EDHXX2	X82198 E. histolyti
c 168	18	1.9	1440	3	AF525293	AF525293 Plasmodiu
c 169	18	1.9	1728	6	AR139606	AR139606 Plasmodium
c 170	18	1.9	1807	3	PFU07365	U07365 Plasmodium
c 171	18	1.9	1886	10	AF411816	AF411816 Mus muscu
c 172	18	1.9	3006	10	BC024690	BC024690 Mus muscu
c 173	18	1.9	4735	10	MUSMUC01	M76179 Mus muscu
c 174	18	1.9	5197	4	RABL51B	D10108 Oryctolagus
c 175	18	1.9	6214	2	AC014611	AC014611 Drosophill
c 176	18	1.9	6833	5	XLCMYC	X53717 X. laevis c-
c 177	18	1.9	9051	2	AC014432	AC014432 Drosophill
c 178	18	1.9	10029	1	AE006274	AE006274 Lactococc
c 179	18	1.9	10078	1	AE006316	AE006316 Lactococc
c 180	18	1.9	10088	1	U32838	U32838 Haemophilus
c 181	18	1.9	10200	10	MMU16175	U16175 Mus muscu
c 182	18	1.9	10244	1	AE006251	AE006251 Lactococc
c 183	18	1.9	10330	1	AE006437	AE006437 Lactococc
c 184	18	1.9	10460	1	AE004248	AE004248 Vibrio ch
c 185	18	1.9	10775	1	AE006296	AE006296 Lactococc
c 186	18	1.9	11255	1	AE006443	AE006443 Lactococc
c 187	18	1.9	11393	1	AE006243	AE006243 Lactococc
c 188	18	1.9	14616	1	BSU09819	U09819 Bacillus su
c 189	18	1.9	18401	8	AY102584	AY102584 Gibberell
c 190	18	1.9	23688	3	U50310	U50310 Caenorhabdi
c 191	18	1.9	29371	1	AF164956	AF164956 Corynebac
c 192	18	1.9	29871	1	LLLPK214	X92946 Lactococcus
c 193	18	1.9	30113	9	HSCN19H5	Z72520 Human DNA s
c 194	18	1.9	30867	2	AC017487	AC017487 Drosophill
c 195	18	1.9	35554	9	HSB3777D9	AL110120 Human DNA
c 196	18	1.9	35618	1	AF080002	AF080002 Helioabaci
c 197	18	1.9	35811	8	SC9718	Z49702 S. cerevisia
c 198	18	1.9	36948	2	AC014499	AC014499 Drosophill
c 199	18	1.9	40676	9	AC000088	AC000088 Homo sapi
c 200	18	1.9	43698	2	AC000071	AC000071 Homo sapi
c 201	18	1.9	50415	2	AC097426	AC097426 Rattus no
c 202	18	1.9	51960	8	AP004983	AP004983 Lotus jap
c 203	18	1.9	51984	2	AC018279	AC018279 Drosophill
c 204	18	1.9	52810	2	AC120420	AC120420 Mus muscu
c 205	18	1.9	53805	9	AL162720	AL162720 Human DNA
c 206	18	1.9	57355	9	AL162720	AL162720 Human DNA
c 207	18	1.9	59303	2	AC015782	AC015782 Homo sapi
c 208	18	1.9	60481	2	AC101780	AC101780 Mus muscu
c 209	18	1.9	62047	2	AC115777	AC115777 Mus muscu
c 210	18	1.9	62934	2	AL112549	AL112549 Rattus no
c 211	18	1.9	63176	9	AL731571	AL731571 Human DNA

C 212	18	1.9	67145	8	AP004920	Lotus jap	285	18	1.9	151806	8	AP002093	Oryza sat
C 213	18	1.9	69070	2	AC100082	Mus muscu	C 286	18	1.9	152010	9	AC026785	Homo sapi
C 214	18	1.9	69172	2	AC129960	Bos tauru	C 287	18	1.9	152238	2	AC119027	Rattus no
C 215	18	1.9	72832	8	AC074228	Arabidops	C 288	18	1.9	152598	2	AC128741	Rattus no
C 216	18	1.9	73021	2	AC017368	Drosophi	C 289	18	1.9	152702	9	AP000237	Homo sapi
C 217	18	1.9	73351	8	AP002057	Arabidops	C 290	18	1.9	152896	2	AC110665	Canis fam
C 218	18	1.9	78917	2	AC018146	AC018146	C 291	18	1.9	152975	2	AC129220	Mus muscu
C 219	18	1.9	81891	9	AC108076	Drosophi	C 292	18	1.9	153160	2	AC110112	Rattus no
C 220	18	1.9	83148	2	AC106381	Rattus no	C 293	18	1.9	153389	2	AC101533	Homo sapi
C 221	18	1.9	85862	3	AC004433	Drosophi	C 294	18	1.9	153556	9	AC004926	Homo sapi
C 222	18	1.9	87124	3	AC004371	Drosophi	C 295	18	1.9	153865	8	AP002744	Oryza sat
C 223	18	1.9	89642	2	AC005136	Homo sapi	C 296	18	1.9	153929	2	AC026023	Homo sapi
C 224	18	1.9	90105	9	AL513007	Human DNA	C 297	18	1.9	153960	2	AC095558	Rattus no
C 225	18	1.9	90170	2	AC098355	Rattus no	C 298	18	1.9	154311	9	AF107258	Homo sapi
C 226	18	1.9	90347	5	AL714030	Zebrafish	C 299	18	1.9	154356	2	AC118518	Rattus no
C 227	18	1.9	96660	9	AL442123	Human DNA	C 300	18	1.9	154597	9	AP004295	Homo sapi
C 228	18	1.9	97348	10	AF091216	Mus muscu	C 301	18	1.9	154793	2	AC016470	Homo sapi
C 229	18	1.9	97433	2	AL512789	Homo sapi	C 302	18	1.9	155424	2	AC129234	Rattus no
C 230	18	1.9	98478	2	AC091370	Rattus no	C 303	18	1.9	155852	2	AC115656	Rattus no
C 231	18	1.9	100000	9	AP000093	Homo sapi	C 304	18	1.9	156777	2	AC114972	Homo sapi
C 232	18	1.9	100000	9	AP000197	Homo sapi	C 305	18	1.9	158347	3	AC092217	Drosophi
C 233	18	1.9	101097	2	AC127438	Rattus no	C 306	18	1.9	158434	9	AL500527	Human DNA
C 234	18	1.9	102382	9	AC007557	Homo sapi	C 307	18	1.9	158706	2	AC128748	Rattus no
C 235	18	1.9	104125	3	AC084468	AC084468	C 308	18	1.9	159096	9	AL161781	Human DNA
C 236	18	1.9	106993	3	AE002751	AE002751	C 309	18	1.9	159693	10	AL646042	Mouse DNA
C 237	18	1.9	108056	8	AC005170	AC005170	C 310	18	1.9	160460	2	AC024374	Homo sapi
C 238	18	1.9	110000	2	AC074222	0	C 311	18	1.9	161221	2	AC126711	Rattus no
C 239	18	1.9	110000	2	AC111011	1	C 312	18	1.9	161428	2	AC126925	Canis fam
C 240	18	1.9	110000	2	AC112266	1	C 313	18	1.9	161536	2	AC024318	Homo sapi
C 241	18	1.9	110000	2	AC129176	1	C 314	18	1.9	161834	2	AC114697	Rattus no
C 242	18	1.9	110000	2	AL139235	1	C 315	18	1.9	161873	8	AC090056	Oryza sat
C 243	18	1.9	110000	2	AL139235	2	C 316	18	1.9	162336	2	AC107170	Rattus no
C 244	18	1.9	110000	2	AL596328	2	C 317	18	1.9	162481	2	AC118954	Homo sapi
C 245	18	1.9	110815	9	AL627260	1	C 318	18	1.9	162680	9	AL158203	Human DNA
C 246	18	1.9	111094	2	AP000683	AP000683	C 319	18	1.9	162760	2	AC079229	Homo sapi
C 247	18	1.9	112283	10	AL732574	AL732574	C 320	18	1.9	163012	3	AC008289	Drosophi
C 248	18	1.9	113515	9	HSJ944FL13	HSJ944FL13	C 321	18	1.9	163641	2	AP005619	Oryza sat
C 249	18	1.9	114741	2	AC111484	AC111484	C 322	18	1.9	163929	2	AC027686	Homo sapi
C 250	18	1.9	116408	2	AC129743	Rattus no	C 323	18	1.9	163958	3	AC010705	Drosophi
C 251	18	1.9	120085	2	AC130016	AC130016	C 324	18	1.9	164035	3	AC007888	Drosophi
C 252	18	1.9	120478	2	AC129844	AC129844	C 325	18	1.9	164049	2	AC126763	Homo sapi
C 253	18	1.9	122947	2	AC162889	AC162889	C 326	18	1.9	164414	3	AC092395	Drosophi
C 254	18	1.9	124048	9	HUAC002045	HUAC002045	C 327	18	1.9	164805	8	OSJN00174	Human DNA
C 255	18	1.9	125577	2	AC109541	AC109541	C 328	18	1.9	165693	9	AC116917	Homo sapi
C 256	18	1.9	126227	2	AC103164	AC103164	C 329	18	1.9	165854	2	AC091539	Canis fam
C 257	18	1.9	129273	2	AC105320	AC105320	C 330	18	1.9	165854	2	AC091539	Canis fam
C 258	18	1.9	130005	9	AL590240	AL590240	C 331	18	1.9	166051	2	AC115126	Rattus no
C 259	18	1.9	130755	2	AC093453	AC093453	C 332	18	1.9	166265	2	AC007841	Homo sapi
C 260	18	1.9	131067	2	AC118536	AC118536	C 333	18	1.9	166368	2	AC127649	Rattus no
C 261	18	1.9	132720	9	AC093269	AC093269	C 334	18	1.9	166849	2	AC127842	Rattus no
C 262	18	1.9	138261	2	AC111740	AC111740	C 335	18	1.9	166869	9	AC016395	Homo sapi
C 263	18	1.9	138490	10	MMU249895	MMU249895	C 336	18	1.9	167480	9	HSBA18114	Human DNA
C 264	18	1.9	138596	2	AC118891	AC118891	C 337	18	1.9	167499	2	CNS01DWX	Homo sapi
C 265	18	1.9	139585	9	AL353786	AL353786	C 338	18	1.9	167981	2	AL591856	Homo sapi
C 266	18	1.9	139649	9	AL359208	AL359208	C 339	18	1.9	168006	9	AC093740	Homo sapi
C 267	18	1.9	139999	8	AC018727	AC018727	C 340	18	1.9	168084	9	AC007037	Homo sapi
C 268	18	1.9	140630	9	AL357514	AL357514	C 341	18	1.9	168438	2	AC024632	Homo sapi
C 269	18	1.9	141756	9	AC024993	AC024993	C 342	18	1.9	168602	2	AF271406	Homo sapi
C 270	18	1.9	142123	9	AC004690	AC004690	C 343	18	1.9	169146	2	AC101797	Mus muscu
C 271	18	1.9	142408	2	AC126338	AC126338	C 344	18	1.9	169340	4	AP001148	Homo sapi
C 272	18	1.9	142616	2	AC067789	AC067789	C 345	18	1.9	169460	4	AL731652	Dog DNA
C 273	18	1.9	144079	2	AC024342	AC024342	C 346	18	1.9	169515	2	AC023213	Homo sapi
C 274	18	1.9	145325	9	AL137789	AL137789	C 347	18	1.9	169649	2	AC046163	Homo sapi
C 275	18	1.9	146582	10	AL662920	AL662920	C 348	18	1.9	170069	9	AC106814	Homo sapi
C 276	18	1.9	147061	2	AC119597	AC119597	C 349	18	1.9	170138	2	AC018794	Homo sapi
C 277	18	1.9	148246	8	AP003054	AP003054	C 350	18	1.9	170339	2	AC128947	Rattus no
C 278	18	1.9	148506	2	AC106345	AC106345	C 351	18	1.9	171029	2	AC096391	Rattus no
C 279	18	1.9	148859	8	OSJN000093	OSJN000093	C 352	18	1.9	171368	9	HSU95738	Human chrom
C 280	18	1.9	149078	2	AC117264	AC117264	C 353	18	1.9	171681	2	AC091541	Canis fam
C 281	18	1.9	149200	9	AL359645	AL359645	C 354	18	1.9	171700	2	AC094677	Rattus no
C 282	18	1.9	149542	9	AC011711	AC011711	C 355	18	1.9	171747	9	AP001554	Homo sapi
C 283	18	1.9	149951	9	AC018375	AC018375	C 356	18	1.9	171972	3	AC012388	Drosophi
C 284	18	1.9	151721	9	AC013265	AC013265	C 357	18	1.9	172367	2	AC118989	Canis fam

C 358	18	1.9	173356	2	AP004047	AP004047	Oryza sat	431	18	1.9	199208	2	AC019236	AC019236	Homo sapi
C 359	18	1.9	173619	2	AC105962	AC105962	Mus muscu	C 432	18	1.9	200964	2	AL732553	AL732553	Mus muscu
C 360	18	1.9	173658	2	AC130996	AC130996	Rattus no	C 433	18	1.9	201410	9	HSF12	HSF12	Homo sapi
C 361	18	1.9	173898	9	AC026886	AC026886	Homo sapi	C 434	18	1.9	201437	2	AC015981	AC015981	Homo sapi
C 362	18	1.9	173904	9	AC025944	AC025944	Homo sapi	C 435	18	1.9	201803	2	AC113572	AC113572	Canis fam
C 363	18	1.9	174375	2	AC026220	AC026220	Homo sapi	C 436	18	1.9	202467	2	AL672232	AL672232	Mus muscu
C 364	18	1.9	174408	2	AC118165	AC118165	Rattus no	C 437	18	1.9	203281	2	AC126237	AC126237	Canis fam
C 365	18	1.9	175054	2	AC018915	AC018915	Homo sapi	C 438	18	1.9	203382	9	AC067854	AC067854	Homo sapi
C 366	18	1.9	175179	2	AC095321	AC095321	Rattus no	C 439	18	1.9	204062	2	AC091072	AC091072	Mus muscu
C 367	18	1.9	175426	2	AC113235	AC113235	Canis fam	C 440	18	1.9	204589	2	AC103655	AC103655	Mus muscu
C 368	18	1.9	176349	8	AP002092	AP002092	Oryza sat	C 441	18	1.9	204731	2	AC009714	AC009714	Homo sapi
C 369	18	1.9	176503	9	AL512604	AL512604	Human DNA	C 442	18	1.9	206160	2	AC113011	AC113011	Mus muscu
C 370	18	1.9	176840	2	AC115024	AC115024	Mus muscu	C 443	18	1.9	206463	2	AP000834	AP000834	Homo sapi
C 371	18	1.9	176840	9	AC105254	AC105254	Homo sapi	C 444	18	1.9	207336	2	AC103907	AC103907	Canis fam
C 372	18	1.9	177018	2	AC106357	AC106357	Rattus no	C 445	18	1.9	207698	9	AC114491	AC114491	Homo sapi
C 373	18	1.9	177108	2	AC026504	AC026504	Homo sapi	C 446	18	1.9	208548	2	AC092195	AC092195	Canis fam
C 374	18	1.9	177108	2	AC026504	AC026504	Homo sapi	C 447	18	1.9	208842	2	AC091295	AC091295	Mus muscu
C 375	18	1.9	177417	2	AC097924	AC097924	Rattus no	C 448	18	1.9	209904	10	AL611984	AL611984	Mouse DNA
C 376	18	1.9	177682	2	AC130050	AC130050	Rattus no	C 449	18	1.9	210496	10	AC104327	AC104327	Mus muscu
C 377	18	1.9	177918	10	AL593855	AL593855	Mouse DNA	C 450	18	1.9	210595	2	AC097034	AC097034	Rattus no
C 378	18	1.9	178067	2	AC130182	AC130182	Rattus no	C 451	18	1.9	211133	2	AC124522	AC124522	Mus muscu
C 379	18	1.9	179052	2	AC094587	AC094587	Rattus no	C 452	18	1.9	211860	2	AC113085	AC113085	Mus muscu
C 380	18	1.9	179596	2	AC094587	AC094587	Rattus no	C 453	18	1.9	212255	2	AC096705	AC096705	Rattus no
C 381	18	1.9	180257	2	AC034164	AC034164	Homo sapi	C 454	18	1.9	213030	2	AC094817	AC094817	Rattus no
C 382	18	1.9	180689	2	AC124913	AC124913	Sus scrof	C 455	18	1.9	213348	2	AC127212	AC127212	Rattus no
C 383	18	1.9	180827	9	AC007344	AC007344	Homo sapi	C 456	18	1.9	213401	10	AL671911	AL671911	Mouse DNA
C 384	18	1.9	180905	2	AC011688	AC011688	Homo sapi	C 457	18	1.9	214425	2	AC092091	AC092091	Canis fam
C 385	18	1.9	181021	2	AL845172	AL845172	Mus muscu	C 458	18	1.9	215286	2	AC111085	AC111085	Mus muscu
C 386	18	1.9	181065	2	AC114891	AC114891	Canis fam	C 459	18	1.9	216692	10	AL671906	AL671906	Mouse DNA
C 387	18	1.9	181542	2	AC121076	AC121076	Canis fam	C 460	18	1.9	218565	3	AC009257	AC009257	Drosophil
C 388	18	1.9	181930	2	AC125614	AC125614	Rattus no	C 461	18	1.9	218904	2	AL844840	AL844840	Mus muscu
C 389	18	1.9	182496	2	AC011190	AC011190	Homo sapi	C 462	18	1.9	220699	2	AC009206	AC009206	Drosophil
C 390	18	1.9	182594	2	AC121853	AC121853	Mus muscu	C 463	18	1.9	222061	2	AC105851	AC105851	Rattus no
C 391	18	1.9	182717	2	AC108399	AC108399	Mus muscu	C 464	18	1.9	222520	10	AC063968	AC063968	Genomic s
C 392	18	1.9	183722	3	AC009341	AC009341	Drosophil	C 465	18	1.9	223373	2	AC122881	AC122881	Mus muscu
C 393	18	1.9	184181	9	AL158141	AL158141	Human DNA	C 466	18	1.9	223624	2	AC093626	AC093626	Homo sapi
C 394	18	1.9	184722	2	AC110668	AC110668	Canis fam	C 467	18	1.9	224076	2	AC084019	AC084019	Mus muscu
C 395	18	1.9	184926	9	AP000757	AP000757	Homo sapi	C 468	18	1.9	225885	9	AC113236	AC113236	Canis fam
C 396	18	1.9	185587	2	AC103935	AC103935	Mus muscu	C 469	18	1.9	227979	9	AC008869	AC008869	Homo sapi
C 397	18	1.9	185666	2	AC048389	AC048389	Homo sapi	C 470	18	1.9	229961	2	AC122919	AC122919	Mus muscu
C 398	18	1.9	185930	2	AC109390	AC109390	Rattus no	C 471	18	1.9	230395	10	AL671878	AL671878	Mouse DNA
C 399	18	1.9	186844	2	AC090052	AC090052	Homo sapi	C 472	18	1.9	238169	2	AC091396	AC091396	Mus muscu
C 400	18	1.9	187349	9	AP003352	AP003352	Human DNA	C 473	18	1.9	240394	2	AC044892	AC044892	Homo sapi
C 401	18	1.9	187908	9	HS495010	HS495010	Human DNA	C 474	18	1.9	246646	2	AL391275	AL391275	Homo sapi
C 402	18	1.9	188216	2	AC092711	AC092711	Mus muscu	C 475	18	1.9	251182	2	AC108230	AC108230	Rattus no
C 403	18	1.9	188674	2	AC114604	AC114604	Mus muscu	C 476	18	1.9	253950	2	AC125085	AC125085	Mus muscu
C 404	18	1.9	188854	10	AL626770	AL626770	Mouse DNA	C 477	18	1.9	254050	1	AL627289	AL627289	Salmonell
C 405	18	1.9	188992	2	AC097896	AC097896	Rattus no	C 478	18	1.9	259744	2	AL844181	AL844181	Mus muscu
C 406	18	1.9	189286	9	AC093906	AC093906	Homo sapi	C 479	18	1.9	261000	3	AE003654	AE003654	Drosophil
C 407	18	1.9	190082	2	AC120136	AC120136	Mus muscu	C 480	18	1.9	264191	2	AC106481	AC106481	Rattus no
C 408	18	1.9	190529	2	AC107732	AC107732	Mus muscu	C 481	18	1.9	264211	2	AC123867	AC123867	Mus muscu
C 409	18	1.9	190724	2	AC078877	AC078877	Homo sapi	C 482	18	1.9	267652	3	AE003577	AE003577	Drosophil
C 410	18	1.9	190743	2	AC073159	AC073159	Homo sapi	C 483	18	1.9	270852	2	AC125346	AC125346	Mus muscu
C 411	18	1.9	192044	9	AL590439	AL590439	Human DNA	C 484	18	1.9	275342	3	AE003649	AE003649	Drosophil
C 412	18	1.9	192235	2	AC025974	AC025974	Homo sapi	C 485	18	1.9	276746	2	AC126670	AC126670	Mus muscu
C 413	18	1.9	193044	10	AC117198	AC117198	Mus muscu	C 486	18	1.9	286963	2	AL732318	AL732318	Mus muscu
C 414	18	1.9	193594	2	AC113281	AC113281	Mus muscu	C 487	18	1.9	295325	3	AE003461	AE003461	Drosophil
C 415	18	1.9	193638	2	AC101886	AC101886	Mus muscu	C 488	18	1.9	300500	1	AP005369	AP005369	Thermosyn
C 416	18	1.9	193641	10	AC121972	AC121972	Mus muscu	C 489	18	1.9	304247	3	AE003452	AE003452	Drosophil
C 417	18	1.9	193995	2	AC127254	AC127254	Mus muscu	C 490	18	1.9	306050	1	RME603645	RME603645	Rhizobium
C 418	18	1.9	194237	9	AC009063	AC009063	Homo sapi	C 491	18	1.9	306450	2	AC068708	AC068708	Homo sapi
C 419	18	1.9	194359	2	AC127720	AC127720	Rattus no	C 492	18	1.9	308092	3	AE003493	AE003493	Drosophil
C 420	18	1.9	194377	2	AC093120	AC093120	Mus muscu	C 493	18	1.9	337178	3	DROSADH08	DROSADH08	Homo sapi
C 421	18	1.9	194602	9	AC113188	AC113188	Homo sapi	C 494	18	1.9	340000	9	AP001706	AP001706	Homo sapi
C 422	18	1.9	195224	2	AC120767	AC120767	Rattus no	C 495	17	1.7	111	9	HS39E8R	HS39E8R	H.sapiens C
C 423	18	1.9	195794	2	AC114924	AC114924	Mus muscu	C 496	17	1.7	117	6	AO6329	AO6329	Hpv18 gene
C 424	18	1.9	196555	2	AC092882	AC092882	Homo sapi	C 497	17	1.7	186	12	SYNAFFG	SYNAFFG	Synthetic f
C 425	18	1.9	196715	2	AC094874	AC094874	Rattus no	C 498	17	1.7	193	6	AR104631	AR104631	Sequence
C 426	18	1.9	197348	2	AC097095	AC097095	Rattus no	C 499	17	1.7	193	6	I38214	I38214	Sequence 44
C 427	18	1.9	197550	9	CNS01RHP	CNS01RHP	Human chr	C 500	17	1.7	344	6	AX208916	AX208916	Sequence
C 428	18	1.9	197870	2	AC091075	AC091075	Homo sapi	C 501	17	1.7	344	6	AX209654	AX209654	Sequence
C 429	18	1.9	198791	2	AC102542	AC102542	Mus muscu	C 502	17	1.7	382	11	G42550	G42550	SHCC-58812
C 430	18	1.9	199046	2	AC126106	AC126106	Rattus no	C 503	17	1.7	387	11	G47478	G47478	Z24974_1_2e

504	17	1.7	402	6	AR137574	AR137574 Sequence	577	17	1.7	2178	5	AB008162	AB008162 Xenopus l
505	17	1.7	402	6	AR139080	AR139080 Sequence	578	17	1.7	2195	9	HSU50436	U50436 Human Down
506	17	1.7	421	11	AF303455	AF303455 Drosophila	C 579	17	1.7	2325	10	AF155196	AF155196 Rattus no
507	17	1.7	449	6	AX198361	AX198361 Sequence	C 580	17	1.7	2327	9	HSU50428	U50428 Human Down
508	17	1.7	477	5	ZEFWHDAB1	L04813 Brachydanio	581	17	1.7	2387	6	I25974	I25974 Sequence 4
509	17	1.7	479	11	AF288327	AF288327 Drosophila	582	17	1.7	2428	9	HSU50439	U50439 Human Down
510	17	1.7	612	6	AX066293	AX066293 Sequence	583	17	1.7	2469	9	AF013274	AF013274 Mus muscu
511	17	1.7	684	10	RNCEH	X60328 R.norvegicu	C 584	17	1.7	2566	9	HSU43378	U43378 Human Down
512	17	1.7	684	10	HS328094	AF120322 Mus muscu	585	17	1.7	2586	10	MMIFNAR2B	Y09864 M.musculus
513	17	1.7	734	9	AX053321	AF328094 Homo sapi	586	17	1.7	2659	10	AF440786	AF440786 Mus muscu
514	17	1.7	747	6	AX053340	AX053321 Sequence	587	17	1.7	2715	10	MMIFNAR2C	Y09865 M.musculus
515	17	1.7	747	6	AX053340	AX053340 Sequence	C 588	17	1.7	2742	4	BOV2PF36G	L42319 Bos taurus
516	17	1.7	756	8	SCYROR83C	Z28308 S.cerevisia	C 589	17	1.7	2884	8	TOMHMG2A	M63642 Tomato 3-hy
517	17	1.7	830	9	HS334408	AF334408 Homo sapi	590	17	1.7	2925	1	PACTOAB	Y10528 P.aeruginos
518	17	1.7	882	10	AF290952	AF290952 Mus muscu	C 591	17	1.7	2965	14	AB067537	AB067537 Norwalk v
519	17	1.7	942	10	AF290953	AF290953 Mus muscu	C 592	17	1.7	2965	14	AB067538	AB067538 Norwalk v
520	17	1.7	963	3	AF205376	AF205376 Plasmodiu	C 593	17	1.7	3019	1	AF270315	AF270315 Staphyloc
521	17	1.7	967	11	CNS066EL	AL395155 17 end of	C 594	17	1.7	3019	6	AX145633	AX145633 Sequence
522	17	1.7	969	6	AX142689	AX142689 Sequence	C 595	17	1.7	3078	3	AF318613	AF318613 Caenorhab
523	17	1.7	969	6	AX143661	AF290954 Mus muscu	596	17	1.7	3129	9	AF077599	AF077599 Homo sapi
524	17	1.7	987	10	AF290954	AF290954 Mus muscu	597	17	1.7	3332	9	AK027409	AK027409 Homo sapi
525	17	1.7	1002	6	E14040	E14040 cDNA encodi	598	17	1.7	3586	8	DGR288901	DGR288901 Dendrobii
526	17	1.7	1104	14	PNE306820	AJ306820 Prunus ne	C 599	17	1.7	3591	8	AB032182	AB032182 Physcomit
527	17	1.7	1105	14	PNE306822	AJ306822 Prunus ne	600	17	1.7	3720	5	XELNCAM	M25696 X.laeviss ne
528	17	1.7	1106	14	PNE306812	AJ306812 Prunus ne	601	17	1.7	3799	6	AX339061	AX339061 Sequence
529	17	1.7	1106	14	PNE306824	AJ306824 Prunus ne	602	17	1.7	3799	9	AF092564	AF092564 Homo sapi
530	17	1.7	1112	6	I15087	I15087 Sequence 1	C 603	17	1.7	3831	2	AC017735	AC017735 Drosophila
531	17	1.7	1113	3	PPARR2	L22058 Plasmodium	C 604	17	1.7	3931	5	AF130459	AF130459 Danio rer
532	17	1.7	1113	5	PGNLDHC4A	L79958 Columbia liv	C 605	17	1.7	3994	9	AL772251	AL772251 Human DNA
533	17	1.7	1146	3	AF404110	AF404110 Junonia c	606	17	1.7	4082	6	AX440472	AX440472 Sequence
534	17	1.7	1185	5	DUKLHDSBCRY	J03869 Duck lactat	607	17	1.7	4086	9	AB019987	AB019987 Homo sapi
535	17	1.7	1209	5	XELRDS38A	L79915 Xenopus lae	608	17	1.7	4093	1	AF269753	AF269753 Staphyloc
536	17	1.7	1233	10	AF290955	AF290955 Mus muscu	609	17	1.7	4093	6	AX145071	AX145071 Sequence
537	17	1.7	1234	5	AF069771	AF069771 Gallus ga	610	17	1.7	4217	8	SPRAD3	X63444 S.pombe rad
538	17	1.7	1240	6	AR050563	AR050563 Sequence	611	17	1.7	4267	8	SCYJL092W	Z49367 S.cerevisia
539	17	1.7	1242	5	L79957	L79957 Columbia liv	612	17	1.7	4660	5	APLDHBD	X68811 A.platyrrhnc
540	17	1.7	1254	8	AF002691	AF002691 Podocarpu	613	17	1.7	4660	5	SCRADH	X15665 Yeast RADH
541	17	1.7	1267	4	SSU95378	U95378 Sus scrofa	C 614	17	1.7	4881	6	BD003805	BD003805 Polynucle
542	17	1.7	1294	5	L79954	L79954 Trachemys s	615	17	1.7	5042	9	HSM805132	AL833949 Homo sapi
543	17	1.7	1295	5	AX163795	AF363795 Pelodiscu	616	17	1.7	5107	6	AX345968	AX345968 Sequence
544	17	1.7	1344	6	AX123416	AX123416 Sequence	C 617	17	1.7	5210	14	HFU89349	U89349 Human papil
545	17	1.7	1345	9	HSM800836	AL10186 Homo sapi	618	17	1.7	5245	1	CBYNNOB	L49438 Chelatoabact
546	17	1.7	1362	10	AF290956	AF290956 Mus muscu	619	17	1.7	5261	9	HSM801845	AL136877 Homo sapi
547	17	1.7	1370	5	AF218799	AF218799 Gallus ga	C 620	17	1.7	5327	9	AY028807	AY028807 Homo sapi
548	17	1.7	1373	3	PFU01322	U01322 Plasmodium	C 621	17	1.7	5416	10	MMU223996	AJ223956 Mus muscu
549	17	1.7	1389	5	XNLNPN038	X56039 X.laeviss mR	C 622	17	1.7	5600	6	AR124758	AR124758 Sequence
550	17	1.7	1404	6	AR120242	AR120242 Sequence	623	17	1.7	5857	1	NMFEDHC	X82637 N.meningiti
551	17	1.7	1404	10	MUSINVO	L28819 Mus musculus	C 624	17	1.7	5932	1	CHU39411	U39411 Chelatoabact
552	17	1.7	1421	6	AX452915	AX452915 Sequence	625	17	1.7	6056	2	AC017797	AC017797 Drosophila
553	17	1.7	1524	6	AR047985	AR047985 Sequence	C 626	17	1.7	6528	9	AB011097	AB011097 Homo sapi
554	17	1.7	1524	6	AR059325	AR059325 Sequence	C 627	17	1.7	6786	10	MMNGA28S	X86000 Mus musculus
555	17	1.7	1528	8	AF152200	AF152200 Libocedru	C 628	17	1.7	7022	10	MMPOLAS6	Y09488 M.musculus
556	17	1.7	1530	8	AF152177	AF152177 Austroced	C 629	17	1.7	7035	3	CELCYTLIA	L26545 Caenorhabdi
557	17	1.7	1552	3	AY051510	AY051510 Drosophila	630	17	1.7	7296	5	AF133907	AF133907 Anolis ca
558	17	1.7	1620	10	AF290957	AF290957 Mus muscu	631	17	1.7	7491	6	AX346487	AX346487 Sequence
559	17	1.7	1638	8	AF351191	AF351191 Zea mays	C 632	17	1.7	7650	2	AC018280	AC018280 Drosophila
560	17	1.7	1640	9	AB070034	AB070034 Macaca fa	C 633	17	1.7	7829	1	RPPLAS	X71612 Buchnera ap
561	17	1.7	1646	14	AF034991	AF034991 Prunus ne	C 634	17	1.7	7857	14	PAPHPV18	X05015 Human papil
562	17	1.7	1652	14	AF034992	AF034992 Prunus ne	C 635	17	1.7	7940	9	HSM804873	AL833560 Homo sapi
563	17	1.7	1653	14	AF034993	AF034993 Prunus ne	636	17	1.7	8022	6	A61387	A61387 Sequence 3
564	17	1.7	1686	14	AF013287	AF013287 Prunus ne	C 637	17	1.7	8022	8	SPRAD3GEN	Y09076 S.pombe RAD
565	17	1.7	1756	9	AK002200	AK002200 Homo sapi	638	17	1.7	8022	8	SPU76307	U76307 Schizosacch
566	17	1.7	1786	3	PFT9PM	W7914 P.falciptaru	C 639	17	1.7	8236	8	SPU66305	U66305 Schizosacch
567	17	1.7	1873	9	HSM804904	AL833591 Homo sapi	C 640	17	1.7	8615	1	AE006711	AE006711 Sulfolobu
568	17	1.7	1950	3	AY095004	AY095004 Drosophila	641	17	1.7	9354	10	RNO18435	Y18435 Rattus norv
569	17	1.7	1951	14	PNRVRN3A	Y07568 Prunus necr	642	17	1.7	9464	8	SJ100567	X77087 S.cerevisia
570	17	1.7	1954	6	AR171283	AR171283 Sequence	C 643	17	1.7	9782	1	AE009941	AE009941 Pyrobacul
571	17	1.7	1957	14	PNU57046	U57046 Prunus necr	C 644	17	1.7	10029	1	AE013368	AE013368 Methanosa
572	17	1.7	1991	9	BC003517	BC003517 Homo sapi	C 645	17	1.7	10299	1	AE004585	AE004585 Pseudomon
573	17	1.7	1992	6	AX402040	AX402040 Sequence	646	17	1.7	10311	1	AE010974	AE010974 Methanosa
574	17	1.7	1992	10	RNCEHR	X65083 R.norvegicu	647	17	1.7	10605	1	AE013050	AE013050 Thermococ
575	17	1.7	2023	10	MMU10484	U10484 Mus musculus	C 648	17	1.7	11342	1	AE003882	AE003882 Xylella f
576	17	1.7	2122	9	HSM800609	AL08105 Homo sapi	649	17	1.7	11353	1	AE007326	AE007326 Streptoco

c 650	17	1.7	11925	9	AC023596	AC023596 Homo sapi	c 723	17	1.7	60555	2	AC100824	AC100824 Homo sapi
c 651	17	1.7	11968	1	AE002482	AE002482 Neisseria	724	17	1.7	60676	2	AC084711	AC084711 Homo sapi
c 652	17	1.7	11976	1	AE006249	AE006249 Pseudococ	725	17	1.7	60815	2	AC100876	AC100876 Mus muscu
c 653	17	1.7	12119	1	AE004810	AE004810 Lactococc	c 726	17	1.7	61204	2	AC017132	AC017132 Drosophil
c 654	17	1.7	12280	1	AE006282	AE006282 Lactococc	727	17	1.7	62214	2	OSIG00034	AL732336 Oryza sat
c 655	17	1.7	13030	1	AE008392	AE008392 Streptoco	c 728	17	1.7	62421	8	NCB3E4	AL355931 Neurospor
c 656	17	1.7	13186	1	AE001613	AE001613 Chlamydia	729	17	1.7	62953	2	AC100701	AC100701 Mus muscu
c 657	17	1.7	13527	1	AE010780	AE010780 Methanosa	c 730	17	1.7	63170	10	AL645799	AL645799 Mouse DNA
c 658	17	1.7	14494	1	AE010475	AE010475 Fusobacte	c 731	17	1.7	63618	2	AC129959	AC129959 Bos tauru
c 659	17	1.7	14960	1	AVU83986	U83986 Agrobacteri	732	17	1.7	64011	9	AC007642	AC007642 Homo sapi
c 660	17	1.7	15758	2	AC014859	AC014859 Drosophil	c 733	17	1.7	64064	2	AC117767	AC117767 Mus muscu
c 661	17	1.7	16310	10	RNO428514	AJ428514 Rattus no	c 734	17	1.7	64478	9	AL603839	AL603839 Human DNA
c 662	17	1.7	16535	2	AC014950	AC014950 Drosophil	c 735	17	1.7	64569	8	AB026650	AB026650 Human DNA
c 663	17	1.7	16652	2	AC018070	AC018070 Drosophil	c 736	17	1.7	64792	9	AL390028	AL390028 Human DNA
c 664	17	1.7	16720	8	LEU68072	U68072 Lycopersico	c 737	17	1.7	64855	2	AC015482	AC015482 Homo sapi
c 665	17	1.7	16766	6	AX347059	AX347059 Sequence	c 738	17	1.7	64873	9	AC108071	AC108071 Homo sapi
c 666	17	1.7	17527	1	AE000098	AE000098 Rhizobium	c 739	17	1.7	64942	2	AC117679	AC117679 Mus muscu
c 667	17	1.7	18002	8	SCUNORF1	Z71116 S.cerevisia	c 740	17	1.7	65034	2	AC016067	AC016067 Homo sapi
c 668	17	1.7	20369	9	AF026276	AF026276 Homo sapi	c 741	17	1.7	65395	2	AC126286	AC126286 Rattus no
c 669	17	1.7	21783	1	AE002208	AE002208 Chlamydo	c 742	17	1.7	65885	9	AL512378	AL512378 Human DNA
c 670	17	1.7	23306	1	AE008747	AE008747 Salmonell	c 743	17	1.7	66668	2	AC102913	AC102913 Mus muscu
c 671	17	1.7	23645	8	SPBC2G5	AL033385 S.pombe c	c 744	17	1.7	66857	2	AC068239	AC068239 Homo sapi
c 672	17	1.7	23919	3	AE003091	AE003091 Drosophil	745	17	1.7	67201	9	AL136169	AL136169 Human DNA
c 673	17	1.7	24206	9	AC128658	AC128658 Homo sapi	c 746	17	1.7	67434	2	AC101255	AC101255 Mus muscu
c 674	17	1.7	25311	8	SPBC216	AL049558 S.pombe c	c 747	17	1.7	67960	2	AC118695	AC118695 Mus muscu
c 675	17	1.7	25416	2	AC013100	AC013100 Drosophil	c 748	17	1.7	68507	2	AC126323	AC126323 Homo sapi
c 676	17	1.7	26411	3	U23486	U23486 Caenorhabdi	c 749	17	1.7	68974	2	AC074063	AC074063 Mus muscu
c 677	17	1.7	28573	3	AF024502	AF024502 Caenorhab	c 750	17	1.7	69096	2	AC121147	AC121147 Mus muscu
c 678	17	1.7	28984	9	AE002059	AE002059 Homo sapi	c 751	17	1.7	69226	2	AC118209	AC118209 Mus muscu
c 679	17	1.7	29034	9	HSA243947	AJ243947 Homo sapi	c 752	17	1.7	69373	2	AC101456	AC101456 Mus muscu
c 680	17	1.7	29158	3	AC119739	AC119739 Homo sapi	c 753	17	1.7	69458	2	AC025432	AC025432 Homo sapi
c 681	17	1.7	29364	3	CBC27B7	Z54236 Caenorhabdi	c 754	17	1.7	69646	2	AC090462	AC090462 Homo sapi
c 682	17	1.7	29498	8	AE023029	AE023029 Arabidops	c 755	17	1.7	69793	9	AC104646	AC104646 Homo sapi
c 683	17	1.7	29552	3	U64845	U64845 Caenorhabdi	c 756	17	1.7	69980	2	AC099820	AC099820 Homo sapi
c 684	17	1.7	31132	8	AB026640	AB026640 Arabidops	c 757	17	1.7	69986	2	AC020283	AC020283 Drosophil
c 685	17	1.7	31441	9	AL592163	AL592163 Human DNA	c 758	17	1.7	70820	8	AP0017451	AP0017451 Drosophil
c 686	17	1.7	31469	3	AF026211	AF026211 Caenorhab	c 759	17	1.7	71184	8	AP001298	AP001298 Arabidops
c 687	17	1.7	33477	3	CET07C4	Z29443 Caenorhabdi	c 760	17	1.7	72137	9	AL356795	AL356795 Human DNA
c 688	17	1.7	33866	2	AC125312	AC125312 Mus muscu	c 761	17	1.7	72198	2	AC123696	AC123696 Mus muscu
c 689	17	1.7	36120	3	U39997	U39997 Caenorhabdi	c 762	17	1.7	73131	2	AC016443	AC016443 Homo sapi
c 690	17	1.7	36949	7	AF2323670	AF2323670 Bacteriop	c 763	17	1.7	73309	2	AL137862	AL137862 Homo sapi
c 691	17	1.7	37482	3	AC024790	AC024790 Caenorhab	c 764	17	1.7	73656	2	AC016512	AC016512 Homo sapi
c 692	17	1.7	38393	9	HSN62C4	Z73963 Human DNA s	c 765	17	1.7	73999	8	AB019226	AB019226 Arabidops
c 693	17	1.7	38490	2	AF001236	AF001236 Homo sapi	c 766	17	1.7	74520	2	AP001264	AP001264 Homo sapi
c 694	17	1.7	38746	2	AC014782	AC014782 Drosophil	c 767	17	1.7	75163	2	AC069103	AC069103 Homo sapi
c 695	17	1.7	38969	3	U51995	U51995 Caenorhabdi	c 768	17	1.7	75245	2	AC101442	AC101442 Mus muscu
c 696	17	1.7	39577	9	AL590671	AL590671 Human DNA	c 769	17	1.7	75647	2	AC101442	AC101442 Mus muscu
c 697	17	1.7	40885	2	AC100188	AC100188 Mus muscu	c 770	17	1.7	76299	2	AC019585	AC019585 Drosophil
c 698	17	1.7	41194	10	AF367979	AF367979 Mus muscu	c 771	17	1.7	77547	2	AC016804	AC016804 Homo sapi
c 699	17	1.7	41623	9	HSN69F4	Z72006 Human DNA s	c 772	17	1.7	77547	2	AC016804	AC016804 Homo sapi
c 700	17	1.7	42338	9	HUMQ16F8	D85922 Human DNA f	c 773	17	1.7	79048	2	AC024976	AC024976 Homo sapi
c 701	17	1.7	42854	9	AF001242	AF001242 Homo sapi	c 774	17	1.7	80204	2	AC016191	AC016191 Homo sapi
c 702	17	1.7	46208	2	AL353712	AL353712 Homo sapi	c 775	17	1.7	80514	9	AC004454	AC004454 Homo sapi
c 703	17	1.7	46864	2	AC100185	AC100185 Mus muscu	c 776	17	1.7	81195	10	AC020807	AC020807 Mus muscu
c 704	17	1.7	48508	9	AC084167	AC084167 Homo sapi	c 777	17	1.7	81195	10	AC091750	AC091750 Mus muscu
c 705	17	1.7	51205	9	AL691465	AL691465 Human DNA	c 778	17	1.7	81255	2	AC017607	AC017607 Drosophil
c 706	17	1.7	51556	9	AL160071	AL160071 Human DNA	c 779	17	1.7	81587	3	AF003135	AF003135 Caenorhab
c 707	17	1.7	51575	8	AF004492	AF004492 Lotus jap	c 780	17	1.7	81672	8	AB020755	AB020755 Arabidops
c 708	17	1.7	51757	8	AC007025	AC007025 Homo sapi	c 781	17	1.7	83823	2	AC006789	AC006789 Caenorhab
c 709	17	1.7	52707	2	AC017288	AC017288 Drosophil	c 782	17	1.7	84234	9	AC107975	AC107975 Homo sapi
c 710	17	1.7	53907	2	AC098773	Continuation (5 of	c 783	17	1.7	84392	2	AC013393	AC013393 Homo sapi
c 711	17	1.7	54527	2	AC015174	AC015174 Drosophil	c 784	17	1.7	84997	2	AC123571	AC123571 Medicago
c 712	17	1.7	55252	2	AC119489	Continuation (4 of	c 785	17	1.7	85432	9	AC099799	AC099799 Homo sapi
c 713	17	1.7	55956	2	AC101559	AC101559 Mus muscu	c 786	17	1.7	85710	8	ATF2809	AL137080 Arabidops
c 714	17	1.7	56733	2	AC017772	AC017772 Drosophil	c 787	17	1.7	85713	9	HSY237C10	Continuation (4 of
c 715	17	1.7	56954	9	AL590663	AL590663 Human DNA	c 788	17	1.7	86298	9	AL355347	AL355347 Human DNA
c 716	17	1.7	57623	2	AC105212	AC105212 Homo sapi	c 789	17	1.7	86323	9	AF445470	AF445470 Homo sapi
c 717	17	1.7	57983	2	AC119877	AC119877 Mus muscu	c 790	17	1.7	86723	9	AF401203	AF401203 Homo sapi
c 718	17	1.7	58433	2	AC100304	AC100304 Mus muscu	c 791	17	1.7	87229	2	AC123538	AC123538 Smnthops
c 719	17	1.7	58641	2	AC104030	AC104030 Homo sapi	c 792	17	1.7	87229	2	AC123538	AC123538 Smnthops
c 720	17	1.7	59261	8	T12M4	AC003114 Arabidops	c 793	17	1.7	87286	2	AC014436	AC014436 Drosophil
c 721	17	1.7	59349	2	AC094968	AC094968 Rattus no	c 794	17	1.7	88413	8	AC005724	AC005724 Arabidops
c 722	17	1.7	59449	2	AC101666	AC101666 Mus muscu	c 795	17	1.7	89297	10	AL606920	AL606920 Mouse DNA

796	17	1.7	89354	9	AC008957	AC008957 Homo sapi	869	17	1.7	112662	9	AC104453	AC104453 Homo sapi
797	17	1.7	89862	9	AC007164	AC007164 Homo sapi	c 870	17	1.7	113284	30	AC074300	AC074300 Homo sapi
798	17	1.7	90289	2	AP003164	AP003164 Homo sapi	c 871	17	1.7	113350	2	AC120244	AC120244 Rattus no
799	17	1.7	91308	2	AC098294	AC098294 Rattus no	c 872	17	1.7	113546	2	HSAC000382	AC000382 Homo sapi
800	17	1.7	91708	2	AC123950_3	Continuation (4 of	873	17	1.7	113951	9	AC007552	AC007552 Homo sapi
c 801	17	1.7	92143	9	HS60898	AL022343 Human DNA	874	17	1.7	114279	2	AC083907	AC083907 Homo sapi
802	17	1.7	92458	9	AC053715	AL121840 Human chr	875	17	1.7	114414	9	AC073073	AC073073 Homo sapi
c 803	17	1.7	93432	9	CNS01DSR	AC0011808 Arabidops	876	17	1.7	114498	8	F309	AC006341 Arabidops
c 804	17	1.7	93485	8	AP004954	AP004954 Lotus jap	877	17	1.7	114656	8	ATT15B3	AL163975 Arabidops
c 805	17	1.7	93645	8	AC004954	AC131393 Homo sapi	878	17	1.7	114793	9	AF217796	AF217796 Homo sapi
c 806	17	1.7	94128	2	AC131393	Z97352 Human DNA s	879	17	1.7	115000	9	AC104831	AC104831 Homo sapi
c 807	17	1.7	94319	9	HS341110	AC1365398 Human DNA	880	17	1.7	115468	2	AC011820	AC011820 Homo sapi
c 808	17	1.7	95298	9	AL365398	AC022385 Homo sapi	c 881	17	1.7	115568	9	AC092120	AC092120 Homo sapi
c 809	17	1.7	96526	2	AC022385	AC106184 Rattus no	c 882	17	1.7	115721	8	F25A4	AC008263 Arabidops
c 810	17	1.7	96640	2	AC106184	AC097401 Rattus no	883	17	1.7	115958	2	AC129038	AC129038 Rattus no
c 811	17	1.7	96671	2	AC097401	AL732325 Human DNA	884	17	1.7	117273	2	AC015138	AC015138 Drosophil
c 812	17	1.7	96764	9	AL732325	AL022171 Human DNA	885	17	1.7	118235	10	AC003060	AC003060 Mus muscu
c 813	17	1.7	96879	9	HS384F21	AL627344 Human DNA	c 886	17	1.7	118780	2	AC097699	AC097699 Rattus no
c 814	17	1.7	97057	9	AL627344	AC013258 Arabidops	887	17	1.7	119028	2	AC098832	AC098832 Oryza sat
c 815	17	1.7	97263	8	AC013258	AC091816 Homo sapi	888	17	1.7	119243	2	AC112576	AC112576 Rattus no
c 816	17	1.7	97860	9	AC091816	AL049651 Human DNA	889	17	1.7	119330	9	AL590076	AL590076 Human DNA
c 817	17	1.7	97860	9	AC091816	AC093085 Homo sapi	c 890	17	1.7	119562	2	AC006779	AC006779 Caenorhab
c 818	17	1.7	97912	9	HSJ753D10	AC111997 Rattus no	891	17	1.7	119821	2	CNS07Y86	AL713929 Oryza sat
c 819	17	1.7	97959	9	AC093085	AL021879 Human DNA	c 892	17	1.7	119972	2	AP004029	AP004029 Oryza sat
c 820	17	1.7	98351	2	AC111997	AC108285 Rattus no	893	17	1.7	120000	2	HSAC000001	AC000001 Homo sapi
c 821	17	1.7	98569	9	HS209B9	AC130096 Rattus no	c 894	17	1.7	120512	9	AL359852	AL359852 Human DNA
c 822	17	1.7	98915	2	AC108285	AC094430 Rattus no	895	17	1.7	120724	2	CNS05TCR	AL355837 Human chr
c 823	17	1.7	99072	2	AC130096	AC056620 Homo sapi	c 896	17	1.7	120780	2	AC095467	AC095467 Rattus no
c 824	17	1.7	99084	2	AC026420	AL355602 Human DNA	c 897	17	1.7	120834	9	AC093602	AC093602 Homo sapi
c 825	17	1.7	99163	9	AL355602	AL11696 Rattus no	898	17	1.7	120864	2	AC128843	AC128843 Rattus no
c 826	17	1.7	103007	2	AC11696	AC069169 Homo sapi	c 899	17	1.7	121027	2	AL157891	AL157891 Homo sapi
c 827	17	1.7	103785	5	AC069169	AC094430 Rattus no	c 900	17	1.7	121151	9	HS705D16	AL034428 Human DNA
c 828	17	1.7	100843	2	AC094430	AL596269 Homo sapi	901	17	1.7	121162	6	AX039602	AX039602 Sequence
c 829	17	1.7	100953	9	AC009489	AL021068 Human DNA	902	17	1.7	122073	2	AC090831	AC090831 Homo sapi
c 830	17	1.7	101427	9	AL596269	AC097932 Rattus no	c 903	17	1.7	122511	2	AC118494	AC118494 Rattus no
c 831	17	1.7	101574	9	HS206D15	AL060732 Zebrafish	c 904	17	1.7	122597	9	AC006062	AC006062 Homo sapi
c 832	17	1.7	101635	2	AC097932	AL064623 Homo sapi	c 905	17	1.7	122844	2	H0719D04	AL442106 Oryza sat
c 833	17	1.7	102735	5	AL606702	AC104407 Homo sapi	906	17	1.7	123369	9	AC025170	AC025170 Homo sapi
c 834	17	1.7	102794	9	AC104623	AC128275 Rattus no	c 907	17	1.7	123436	9	AC009872	AC009872 Homo sapi
c 835	17	1.7	102822	9	AC104407	AL353814 Arabidops	c 908	17	1.7	123764	2	OSJN000097	AL606650 Oryza sat
c 836	17	1.7	102848	2	AC128275	AC108975 Rattus no	909	17	1.7	124040	2	AC097412	AC097412 Rattus no
c 837	17	1.7	102873	8	ATF26G5	AC007153 Arabidops	910	17	1.7	124114	9	HSJ858M22	AL118510 Human DNA
c 838	17	1.7	103211	2	AC106975	AL139175 Human DNA	c 911	17	1.7	124696	2	AP000649	AP000649 Homo sapi
c 839	17	1.7	103223	8	AC007153	AL355810 Human DNA	c 912	17	1.7	124912	2	AC129811	AC129811 Rattus no
c 840	17	1.7	103718	9	AL139175	AC128003 Rattus no	c 913	17	1.7	125086	9	AL607044	AL607044 Human DNA
c 841	17	1.7	103749	9	AL355810	AC123021 Homo sapi	c 914	17	1.7	125198	2	AP004329	AP004329 Rattus no
c 842	17	1.7	104129	2	AC128003	AC093288 Homo sapi	c 915	17	1.7	125346	2	AP000367	AP000367 Oryza sat
c 843	17	1.7	104395	2	AC123021	AL035594 Human DNA	916	17	1.7	126038	8	AC103657	AC103657 Mus muscu
c 844	17	1.7	104895	2	AC093288	AL672107 Zebrafish	917	17	1.7	126046	2	AC103657	AC103657 Mus muscu
c 845	17	1.7	105100	9	HS67A5	AC111925 Rattus no	c 918	17	1.7	126046	2	AC123141	AC123141 Rattus no
c 846	17	1.7	106684	5	AL672107	AC121711 Rattus no	c 919	17	1.7	126707	2	AL603882	AL603882 Human DNA
c 847	17	1.7	106928	2	AC111925	AC094316 Rattus no	c 920	17	1.7	126779	2	AL138904	AL138904 Homo sapi
c 848	17	1.7	108449	2	AC121711	AL359185 Human DNA	921	17	1.7	127119	2	AC123277	AC123277 Rattus no
c 849	17	1.7	108456	2	AC094316	AL162379 Human DNA	922	17	1.7	127199	2	AC123277	AC123277 Rattus no
c 850	17	1.7	108841	9	AL359185	Continuation (2 of	923	17	1.7	127399	9	AL158825	AL158825 Human DNA
c 851	17	1.7	109288	9	AL359081	Continuation (3 of	c 924	17	1.7	127439	9	AC126178	AC126178 Homo sapi
c 852	17	1.7	109757	9	AL162379	Continuation (5 of	c 925	17	1.7	127713	2	OSJN00007	AL606452 Oryza sat
c 853	17	1.7	110000	2	AC091454_1	Continuation (5 of	c 926	17	1.7	128167	10	AL806526	AL806526 Mouse DNA
c 854	17	1.7	110000	2	AC122571_2	Continuation (5 of	c 927	17	1.7	128228	9	AL138810	AL138810 Human DNA
c 855	17	1.7	110000	2	AC125066_4	Continuation (4 of	928	17	1.7	128228	2	HS2298105	AJ298105 Homo sapi
c 856	17	1.7	110000	2	AL353584_0	Continuation (3 of	c 929	17	1.7	128228	2	AC128115	AC128115 Rattus no
c 857	17	1.7	110000	2	AL672265_0	Continuation (3 of	c 930	17	1.7	128493	2	AC109964	AC109964 Rattus no
c 858	17	1.7	110000	2	LMFLCHR18_04	Continuation (5 of	c 931	17	1.7	128600	9	AC005192	AC005192 Homo sapi
c 859	17	1.7	110000	2	LMFLCHR31_00	Continuation (12 of	932	17	1.7	128815	2	AL773559	AL773559 Sus scrofa
c 860	17	1.7	110000	2	LMFLCHR32_11	Continuation (4 of	c 933	17	1.7	128915	2	AL126000	AL126000 Rattus no
c 861	17	1.7	110000	2	AC055726_3	Continuation (3 of	934	17	1.7	128968	9	AL356858	AL356858 Human DNA
c 862	17	1.7	110000	9	HSY237C10_2	Continuation (3 of	c 935	17	1.7	129096	2	AC026412	AC026412 Homo sapi
c 863	17	1.7	110898	9	AL355973	AC114337 Homo sapi	c 936	17	1.7	129992	9	AL354897	AL354897 Human DNA
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c 865	17	1.7	111104	9	AC117389	AC013451 Homo sapi	938	17	1.7	130754	2	AC008508	AC008508 Homo sapi
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c 868	17	1.7	111762	9	AC103851		941	17	1.7	132035	2	AC125548	AC125548 Rattus no
c 869	17	1.7	112180	9	HSJ322G13								

942	17	1-7	132147	2	AC125826	AC125826	Rattus no
c 943	17	1-7	132171	3	AC008370	AC008370	Drosophil
944	17	1-7	132614	10	AC021756	AC021756	Mus muscu
945	17	1-7	132710	9	AC093535	AC093535	Homo sapi
946	17	1-7	132878	2	AC108187	AC108187	Felis cat
947	17	1-7	132953	9	AC024221	AC024221	Homo sapi
c 948	17	1-7	133294	2	AC118310	AC118310	Rattus no
949	17	1-7	133418	9	AL353709	AL353709	Human DNA
c 950	17	1-7	133477	10	AL646091	AL646091	Mouse DNA
c 951	17	1-7	133730	2	AC104294	AC104294	Rattus no
952	17	1-7	133789	9	AL442126	AL442126	Human DNA
953	17	1-7	133790	9	AC010280	AC010280	Homo sapi
954	17	1-7	134019	3	AC006471	AC006471	Drosophil
c 955	17	1-7	134250	9	AL133044	AL133044	Human DNA
956	17	1-7	134506	9	HS357116	HS357116	Homo sapi
957	17	1-7	134518	2	OSJN00134	OSJN00134	Homo sapi
958	17	1-7	135062	9	AC026691	AC026691	Oryza sat
959	17	1-7	135584	2	AC125496	AC125496	Oryza sat
c 960	17	1-7	136093	2	AC067894	AC067894	Homo sapi
961	17	1-7	136219	9	AP000697	AP000697	Homo sapi
c 962	17	1-7	137217	2	HS4211140	HS4211140	Homo sapi
963	17	1-7	137586	9	AC106775	AC106775	Homo sapi
c 964	17	1-7	137740	1	D90900	D90900	Synechocyst
965	17	1-7	138604	9	AC104826	AC104826	Homo sapi
966	17	1-7	138616	2	AC115525	AC115525	Rattus no
c 967	17	1-7	138982	2	AC104550	AC104550	Mus muscu
c 968	17	1-7	139218	2	AC019289	AC019289	Homo sapi
c 969	17	1-7	139290	2	AC068096	AC068096	Homo sapi
970	17	1-7	139924	2	AC116512	AC116512	Mus muscu
c 971	17	1-7	140774	2	AC108904	AC108904	Felis cat
c 972	17	1-7	140949	9	AC117339	AC117339	Rattus no
c 973	17	1-7	141120	9	AC002528	AC002528	Human BAC
974	17	1-7	141670	9	AC104170	AC104170	Homo sapi
975	17	1-7	141815	9	AC112716	AC112716	Homo sapi
976	17	1-7	142017	2	HS4196H18	HS4196H18	Homo sapi
c 977	17	1-7	142085	2	AC036153	AC036153	Homo sapi
978	17	1-7	142143	2	AC129352	AC129352	Homo sapi
c 979	17	1-7	142195	2	AC010669	AC010669	Drosophil
c 980	17	1-7	142388	2	AC128446	AC128446	Rattus no
981	17	1-7	142478	2	AC106966	AC106966	Rattus no
c 982	17	1-7	142837	2	AC113323	AC113323	Canis fam
983	17	1-7	142955	8	AP003349	AP003349	Oryza sat
984	17	1-7	143062	2	AC109092	AC109092	Rattus no
c 985	17	1-7	143264	2	AC119547	AC119547	Rattus no
c 986	17	1-7	143418	2	AC130228	AC130228	Rattus no
c 987	17	1-7	143534	2	AC036128	AC036128	Homo sapi
988	17	1-7	143611	9	AC068992	AC068992	Homo sapi
c 989	17	1-7	143676	2	AC026435	AC026435	Homo sapi
c 990	17	1-7	143684	2	AC107323	AC107323	Felis cat
c 991	17	1-7	143879	2	AC130724	AC130724	Oryza sat
c 992	17	1-7	144000	9	AC007621	AC007621	Homo sapi
c 993	17	1-7	144328	9	AC009695	AC009695	Homo sapi
c 994	17	1-7	144514	2	AC115534	AC115534	Sus scrof
c 995	17	1-7	144609	9	AC021269	AC021269	Homo sapi
996	17	1-7	144675	2	AC116060	AC116060	Rattus no
c 997	17	1-7	144724	8	AC078948	AC078948	Oryza sat
c 998	17	1-7	144967	2	AC008963	AC008963	Homo sapi
c 999	17	1-7	145216	3	AC092224	AC092224	Drosophil
1000	17	1-7	145265	8	AP003418	AP003418	Oryza sat

ALIGNMENTS

RESULT 1
AC113646/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-324G7, *** SEQUENCING IN PROGRESS
*** 35 unordered pieces.
AC113646
AC113646
AC113646.3 GI:21738663
HTG; HTGS_PHASE1.
Norway rat.

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
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Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
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Usmani, K., Vazquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
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Williams, G., Williamson, A., Wleczky, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission

Unpublished

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Consensus quality: 126566 bases at least Q30
Consensus quality: 129561 bases at least Q20

NOTE: Estimated insert size may differ from sequence length
(see http://www.hqsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 35 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1002: contig of 1002 bp in length
1003 1102: gap of unknown length
1103 2439: contig of 1337 bp in length
2440 2539: gap of unknown length
2540 3615: contig of 1076 bp in length
3616 3715: gap of unknown length
3716 5109: contig of 1394 bp in length
5110 5209: gap of unknown length
5210 6650: contig of 1441 bp in length
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6751 8244: contig of 1494 bp in length
8245 9594: gap of unknown length
9595 9694: gap of unknown length
9695 11425: contig of 1731 bp in length
11426 11525: gap of unknown length
11526 13702: contig of 2177 bp in length
13703 13802: gap of unknown length
13803 16415: contig of 2613 bp in length
16416 16515: gap of unknown length
16516 18030: contig of 1515 bp in length
18031 18130: gap of unknown length
18131 20346: contig of 2116 bp in length
20347 22138: gap of unknown length
22139 22238: gap of unknown length
22239 24024: contig of 1786 bp in length
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27114 27213: gap of unknown length
27214 30060: contig of 2847 bp in length
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103726 103825: gap of unknown length

103826 110175: contig of 6350 bp in length
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118451 118550: gap of unknown length
118551 129915: contig of 11265 bp in length
129916 129915: gap of unknown length
129916 139145: contig of 9230 bp in length
139146 139245: gap of unknown length
139246 151778: contig of 12533 bp in length.

FEATURES

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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-324G7"

BASE COUNT 43201 a 29596 c 29588 g 45822 t 3571 others
ORIGIN

Query Match 2.4%; Score 23; DB 2; Length 151778;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 TCCTACCAAACTCAATAAAAGT 867

Db 32134 TCCTACCAAACTCAATAAAAGT 32112

RESULT 2

AC099573

LOCUS

DEFINITION

AC099573

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AC099573 214265 bp DNA linear HTG 20-AUG-2002
Mus musculus clone RP23-28E6, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
AC099573 GI:232325167
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome, clone RP23-28E6
Unpublished
2 (bases 1 to 214265)

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JOURNAL

REFERENCE

AUTHORS

Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 214265)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

```

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 20, 2002 this sequence version replaced gi:16946021.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13795
Center clone name: 28_E_6
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 213019 bases at least Q40
Consensus quality: 213493 bases at least Q30
Consensus quality: 213665 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 213865; sum-of-contigs
Quality coverage: 14.5 in Q20 bases; agarose-fp
Quality coverage: 14.3 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 16219: contig of 16219 bp in length
* 16220 16319: gap of 100 bp
* 16320 120317: contig of 10398 bp in length
* 120318 120417: gap of 100 bp
* 120418 163351: contig of 42934 bp in length
* 163352 163451: gap of 100 bp
* 163452 210716: contig of 47265 bp in length
* 210717 210816: gap of 100 bp
* 210817 214265: contig of 3449 bp in length.
*
* Location/Qualifiers
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* 1. .214265
* /organism="Mus musculus"
* /db_xref="taxon:10090"
* /clone="RP23-28E6"
* /clone_lib="RPCI-23 Female Mouse BAC"
*
* 1. .16219
* /note="assembly_fragment"
* clone_end:SP6
* vector_side:left
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* 16320-120317
* /note="assembly_fragment"
*
* 120418-163351
* /note="assembly_fragment"
*
* 163452-210716

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/note="assembly_fragment"
210817-214265
/notes="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 72086 a 41630 c 41065 g 59084 t 400 others
ORIGIN

Query Match 2.3%; Score 22; DB 2; Length 214265;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 GTGGGATTAAACCAAAAAAATGG 287
|||||
Db 160881 GTGGGATTAAACCAAAAAAATGG 160902

RESULT 3
AC114589/c
LOCUS
AC114589
DEFINITION Mus musculus clone RP23-365013, LOW-PASS SEQUENCE SAMPLING.
AC114589
VERSION AC114589.1 GI:19311117
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 62004)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-365013
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 62004)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lakocue,K., Lamazares,R.,
Landers,T., Lehocsky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23822
Center clone name: 365_O_13
-----
* NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads

```

* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 704: contig of 704 bp in length
* 705 804: gap of 100 bp
* 805 1480: contig of 676 bp in length
* 1481 1580: gap of 100 bp
* 1581 2282: contig of 702 bp in length
* 2283 2382: gap of 100 bp
* 2383 3090: contig of 708 bp in length
* 3091 3190: gap of 100 bp
* 3191 3845: contig of 656 bp in length
* 3847 3946: gap of 100 bp
* 3947 4663: contig of 717 bp in length
* 4664 4763: gap of 100 bp
* 4764 5456: contig of 693 bp in length
* 5457 5556: gap of 100 bp
* 5557 6248: contig of 692 bp in length
* 6249 6348: gap of 100 bp
* 6349 7061: contig of 713 bp in length
* 7062 7161: gap of 100 bp
* 7162 7865: contig of 704 bp in length
* 7866 7965: gap of 100 bp
* 7966 8679: contig of 714 bp in length
* 8680 8779: gap of 100 bp
* 8780 9484: contig of 705 bp in length
* 9485 9584: gap of 100 bp
* 9585 10300: contig of 716 bp in length
* 10301 10400: gap of 100 bp
* 10401 11103: contig of 709 bp in length
* 11104 11209: gap of 100 bp
* 11210 11914: contig of 705 bp in length
* 11915 12014: gap of 100 bp
* 12015 12713: contig of 699 bp in length
* 12714 12813: gap of 100 bp
* 12814 13523: contig of 710 bp in length
* 13524 13623: gap of 100 bp
* 13624 14333: contig of 710 bp in length
* 14334 14433: gap of 100 bp
* 14434 15147: contig of 714 bp in length
* 15148 15247: gap of 100 bp
* 15248 15951: contig of 704 bp in length
* 15952 16051: gap of 100 bp
* 16052 16774: contig of 723 bp in length
* 16775 16874: gap of 100 bp
* 16875 17579: contig of 705 bp in length
* 17580 17679: gap of 100 bp
* 17680 18398: contig of 719 bp in length
* 18399 18498: gap of 100 bp
* 18499 19212: contig of 714 bp in length
* 19213 19312: gap of 100 bp
* 19313 20021: contig of 709 bp in length
* 20022 20121: gap of 100 bp
* 20122 20834: contig of 713 bp in length
* 20835 20934: gap of 100 bp
* 20935 21645: contig of 711 bp in length
* 21646 21745: gap of 100 bp
* 21746 22454: contig of 709 bp in length
* 22455 22554: gap of 100 bp
* 22555 23225: contig of 703 bp in length
* 23258 23357: gap of 100 bp
* 23358 24008: contig of 651 bp in length
* 24009 24108: gap of 100 bp
* 24109 24812: contig of 704 bp in length
* 24813 24912: contig of 100 bp
* 24913 25625: contig of 713 bp in length
* 25626 25725: gap of 100 bp
* 25726 26449: contig of 724 bp in length

* 26450 26549: gap of 100 bp
* 26550 27257: contig of 708 bp in length
* 27258 27357: gap of 100 bp
* 27358 28069: contig of 712 bp in length
* 28070 28169: gap of 100 bp
* 28170 28864: contig of 695 bp in length
* 28865 28964: gap of 100 bp
* 28965 29675: contig of 711 bp in length
* 29676 29775: gap of 100 bp
* 29776 30477: contig of 702 bp in length
* 30478 30577: gap of 100 bp
* 30578 31292: contig of 715 bp in length
* 31293 31392: gap of 100 bp
* 31393 32112: contig of 720 bp in length
* 32113 32212: gap of 100 bp
* 32213 32919: contig of 707 bp in length
* 32920 33019: gap of 100 bp
* 33020 33735: contig of 716 bp in length
* 33736 33835: gap of 100 bp
* 33836 34547: contig of 712 bp in length
* 34548 34647: gap of 100 bp
* 34648 35354: contig of 707 bp in length
* 35355 35454: gap of 100 bp
* 35455 36127: contig of 673 bp in length
* 36128 36227: gap of 100 bp
* 36228 36940: contig of 713 bp in length
* 36941 37040: gap of 100 bp
* 37041 37751: contig of 711 bp in length
* 37752 37851: gap of 100 bp
* 37852 38545: contig of 694 bp in length
* 38546 38645: gap of 100 bp
* 38646 39357: contig of 712 bp in length
* 39358 39457: gap of 100 bp
* 39458 40157: contig of 700 bp in length
* 40158 40257: gap of 100 bp
* 40258 40972: contig of 715 bp in length
* 40973 41072: gap of 100 bp
* 41073 41791: contig of 719 bp in length
* 41792 41891: gap of 100 bp
* 41892 42599: contig of 708 bp in length
* 42600 42699: gap of 100 bp
* 42700 43402: contig of 703 bp in length
* 43403 43502: gap of 100 bp
* 43503 44211: contig of 709 bp in length
* 44212 44311: gap of 100 bp
* 44312 45024: contig of 713 bp in length
* 45025 45124: gap of 100 bp
* 45125 45835: contig of 711 bp in length
* 45836 45935: gap of 100 bp
* 45936 46639: contig of 704 bp in length
* 46640 46739: gap of 100 bp
* 46740 47452: contig of 713 bp in length
* 47453 47552: gap of 100 bp
* 47553 48255: contig of 703 bp in length
* 48256 48355: gap of 100 bp
* 48356 49078: contig of 723 bp in length
* 49079 49178: gap of 100 bp
* 49179 49899: contig of 721 bp in length
* 49900 49999: gap of 100 bp
* 50000 50716: contig of 717 bp in length
* 50717 50816: gap of 100 bp
* 50817 51528: contig of 712 bp in length
* 51529 51628: gap of 100 bp
* 51629 52338: contig of 710 bp in length
* 52339 52438: gap of 100 bp
* 52439 53146: contig of 708 bp in length
* 53147 53246: gap of 100 bp
* 53247 53959: contig of 713 bp in length
* 53960 54059: gap of 100 bp
* 54060 54762: contig of 703 bp in length
* 54763 54862: gap of 100 bp
* 54863 55547: contig of 685 bp in length
* 55548 55647: gap of 100 bp

Query Match 2.2%; Score 21; DB 2; Length 62004;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 626 AAAAAGCCACCATATTTG 646
 Db 56146 AAAAAGCCACCATATTTG 56126

RESULT 4
 AL355985/c
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-98017 on chromosome 9, complete sequence.
 ACCESSION AL355985
 VERSION AL355985.18 GI:16972867
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 64969)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Direct Submission
 JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquyes@sanger.ac.uk

COMMENT On Nov 16, 2001 this sequence version replaced gi:16416171. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; the following assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr9
 RP11-98017 is from the library RPCI-11.1 constructed by the group of Peter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-98017 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-388B24 is at 62970 in this sequence. The true right end of clone RP11-383M4 is at 2000 in this sequence.

FEATURES
 source
 1..64969
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="9"
 /clone="RP11-98017"
 /clone_lib="RPCI-11.1"
 BASE COUNT 18132 a 13055 c 13036 g 20746 t
 ORIGIN

Query Match 2.2%; Score 21; DB 9; Length 64969;
 Best Local Similarity 100.0%; Pred. No. 6.5;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 898 GATGAGAGCAATGATTTG 918
 Db 41352 GATGAGAGCAATGATTTG 41332

RESULT 5
 AC087568
 LOCUS
 DEFINITION Pan troglodytes clone RP43-135M11, complete sequence.
 ACCESSION AC087568
 VERSION AC087568.2 GI:16596569
 KEYWORDS HTG.
 SOURCE Pan troglodytes.

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 150199)
 AUTHORS Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantropop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgou, C., Vogt, J.B., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.

TITLE NISC Comparative Sequencing Initiative
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 150199)
 AUTHORS Green, E.D.

TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2001) NIH Intramural Sequencing Center, 8717

REFERENCE 3 (bases 1 to 150199)
 AUTHORS Green, E.D.

TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2001) NIH Intramural Sequencing Center, 8717

COMMENT On Nov 2, 2001 this sequence version replaced gi:12061434.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: http://www.nisc.nih.gov
 Contact: nisc_mouse@nigri.nih.gov
 ----- Project Information
 Center project name: agf
 Center clone name: 135M11

This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features section.
 Location/Qualifiers
 1..150199
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="RP43-135M11"
 /clone_lib="RP43"
 BASE COUNT 36501 a 36322 c 37037 g 40339 t
 ORIGIN

Query Match 2.2%; Score 21; DB 9; Length 150199;

Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 401 ATGTTTGGACCTATTAGCT 421
Db 79411 ATGTTTGGACCTATTAGCT 79431

RESULT 6
AC111597
LOCUS
DEFINITION Rattus norvegicus clone CH230-150P11, *** SEQUENCING IN PROGRESS
***, 62 unordered pieces.
AC111597
VERSION AC111597.2 GI:21736155
KEYWORDS HTG; HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 169574)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alshrooks, S.L., Amarantunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
DeLaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karleson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, D.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louleghed, H.,
Lozados, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshkari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 169574)
Worley, K.C.
Direct Submission
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 169574)
Worley, K.C.
Direct Submission
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18701364.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMOL
Center clone name: CH230-150P11
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113501 bases at least Q40
Consensus quality: 119212 bases at least Q30
Consensus quality: 124054 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1
1152: contig of 1152 bp in length
1153 1252: gap of unknown length
1253 2646: contig of 1394 bp in length
2647 2747: gap of unknown length
2747 4284: contig of 1538 bp in length
4285 4384: gap of unknown length
4385 5330: contig of 1046 bp in length
5331 5530: gap of unknown length
5531 6683: contig of 1152 bp in length
6683 6782: gap of unknown length
6783 8328: contig of 1546 bp in length
8329 8429: gap of unknown length
8429 9655: contig of 1226 bp in length
9655 9755: gap of unknown length
9755 11055: contig of 1301 bp in length
11056 12880: contig of 1125 bp in length
12881 13455: contig of 1075 bp in length
13456 15071: contig of 1516 bp in length
15072 15171: gap of unknown length
15172 16403: contig of 1232 bp in length
16404 17702: contig of 1198 bp in length
17702 19484: contig of 1683 bp in length
19485 21722: contig of 1588 bp in length
21723 22768: contig of 1496 bp in length
22769 24002: contig of 1134 bp in length
24003 25337: contig of 1435 bp in length
25338 25638: gap of unknown length
25639 27003: contig of 1266 bp in length
27004 28985: contig of 1982 bp in length
28986 31277: contig of 2192 bp in length
31278 33368: contig of 1991 bp in length
33369

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* 33369 33468: gap of unknown length
* 33469 34518: contig of 1050 bp in length
* 34519 34618: gap of unknown length
* 34619 34688: contig of 1870 bp in length
* 34689 36588: gap of unknown length
* 36589 38145: contig of 1557 bp in length
* 38146 38245: gap of unknown length
* 38246 38774: contig of 1529 bp in length
* 38775 39874: gap of unknown length
* 39875 41463: contig of 1589 bp in length
* 41464 42961: gap of unknown length
* 42962 43061: contig of 1398 bp in length
* 43062 45065: contig of 2004 bp in length
* 45066 45165: gap of unknown length
* 45166 47102: contig of 1937 bp in length
* 47103 47202: gap of unknown length
* 47203 49519: contig of 2317 bp in length
* 49520 49619: gap of unknown length
* 49620 51310: contig of 1691 bp in length
* 51311 51410: gap of unknown length
* 51411 52960: contig of 1550 bp in length
* 52961 53061: gap of unknown length
* 53062 55201: contig of 2141 bp in length
* 55202 55301: gap of unknown length
* 55302 57573: contig of 2272 bp in length
* 57574 57673: gap of unknown length
* 57674 60208: contig of 2535 bp in length
* 60209 60308: gap of unknown length
* 60309 62351: contig of 2043 bp in length
* 62352 64551: gap of unknown length
* 64552 64851: contig of 2400 bp in length
* 64852 64951: gap of unknown length
* 64952 67104: contig of 2153 bp in length
* 67105 67204: gap of unknown length
* 67205 69433: contig of 2229 bp in length
* 69434 69533: gap of unknown length
* 69534 72227: contig of 2693 bp in length
* 72228 72326: gap of unknown length
* 72327 76213: contig of 3887 bp in length
* 76214 76313: gap of unknown length
* 76314 78709: contig of 2396 bp in length
* 78710 78809: gap of unknown length
* 78810 81500: contig of 2691 bp in length
* 81501 81600: gap of unknown length
* 81601 84321: contig of 2721 bp in length
* 84322 84422: gap of unknown length
* 84423 87220: contig of 2799 bp in length
* 87221 87320: gap of unknown length
* 87321 92378: contig of 5058 bp in length
* 92379 92478: gap of unknown length
* 92479 95106: contig of 2628 bp in length
* 95107 95206: gap of unknown length
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* 101793 104836: contig of 3044 bp in length
* 104837 104936: gap of unknown length
* 104937 110703: contig of 5767 bp in length
* 110704 110803: gap of unknown length
* 110804 113760: contig of 2957 bp in length
* 113761 113861: gap of unknown length
* 113862 118784: contig of 4924 bp in length

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Query Match 2.2%; Score 21; DB 2; Length 169574;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 AAGACAAAGCAGAGGTCGAAA 172

Db 3741 AAGACAAAGCAGAGGTCGAAA 3761

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RESULT 7
AC091001 177066 bp DNA linear PRI 06-DEC-2001
LOCUS Papio cynocephalus anubis clone RP41-36M16, complete sequence.
DEFINITION AC091001
ACCESSION AC091001
VERSION AC091001.2 GI:17386264
KEYWORDS HTG.
SOURCE Papio cynocephalus anubis.
ORGANISM Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 177066)
AUTHORS Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-O.,
Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y.,
Scantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
Tsurgoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
UNPUBLISHED
REFERENCE 2 (bases 1 to 177066)
AUTHORS Green,E.D.
DIRECT SUBMISSION
TITLE Submitted (26-MAR-2001) NIH Intramural Sequencing Center, 8717
JOURNAL Grovmont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 177066)
AUTHORS Green,E.D.
DIRECT SUBMISSION
TITLE Submitted (06-DEC-2001) NIH Intramural Sequencing Center, 8717
JOURNAL Grovmont Circle, Gaithersburg, MD 20877, USA
COMMENT On Dec 6, 2001 this sequence version replaced gi:13447439.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@nhgri.nih.gov
----- Project Information
Center project name: asg
Center clone name: 036M16

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This sequence was finished as follows unless otherwise noted:
 all regions were double-stranded, sequenced with an
 alternate chemistry, or covered by high quality data
 (i.e., phred quality >= 30); an attempt was made to resolve
 all sequencing problems, such as compressions and repeats;
 all regions were covered by at least one plasmid subclone
 or more than one M13 subclone; and the assembly was confirmed
 by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of
 this clone unless otherwise noted. If there are overlapping
 clones, the overlaps are noted in the beginning and end of
 the Features section.

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FEATURES
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    /db_xref="taxon:9555"
    /clone="RP41-36M16"
    /clone_lib="RP41"
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    /note="single clone coverage"
misc_feature
  3862..4236
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  82768..82855
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/note="single clone coverage"
93063. .93191
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94176. .94491
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142486. 142509
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42959 a 42842 c 44880 g 46385 t
BASE COUNT
ORIGIN

Query Match      2.2%  Score 21;  DB 9;  Length 177066;
Best Local Similarity 100.0%;  Pred. No. 6.3;
Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  401 ATGTTTGACCTATATTAGCT 421
    |||||
Db  100974 ATGTTTGACCTATATTAGCT 100994

RESULT 8
AC005089
LOCUS      177893 bp  DNA  linear  PRI 30-MAR-2002
DEFINITION Homo sapiens BAC clone CTA-315H11 from 7q11.2, complete sequence.
ACCESSION  AC005089
VERSION     AC005089.3  GI:19747251
KEYWORDS   HTG.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 177893)
AUTHORS   Sulston, J.E. and Waterston, R.
TITLE     Toward a complete human genome sequence
JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE   99063792
PUBMED    9847074
REFERENCE  2 (bases 1 to 177893)
AUTHORS   Graves, T., Maas, J. and Hawkins, M.
TITLE     The sequence of Homo sapiens BAC clone CTA-315H11
JOURNAL   Unpublished (2001)
REFERENCE  3 (bases 1 to 177893)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  4 (bases 1 to 177893)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (13-AUG-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  5 (bases 1 to 177893)
AUTHORS   Waterston, R.
TITLE     Direct Submission
JOURNAL   Submitted (02-OCT-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE  6 (bases 1 to 177893)
AUTHORS   Waterston, R.H.
TITLE     Direct Submission
JOURNAL   Submitted (27-MAR-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE  7 (bases 1 to 177893)
AUTHORS   Waterston, R.
TITLE     Direct Submission
JOURNAL   Submitted (30-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT    On Mar 27, 2002 this sequence version replaced gi:5732140.
            ----- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc

```

Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics
 Center project name: H_RG315H11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GT8/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

Clone CTA-315H11 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
 VECTOR: pBelOBAC11
 Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RG208H19. Actual start of this clone is at base position 1 of RG315H11; actual end is at base position 177893 of RG315H11.

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repeat_region	613. 910
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repeat_region	948. 1044
repeat_region	/rpt_family="MIR"
repeat_region	1016. 1515
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repeat_region	1260. 1317
repeat_region	/rpt_family="GA-rich"
repeat_region	1431. 1733
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Query Match 2.2%; Score 21; DB 9; Length 177893;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 ATGTTTGACCTATTAGCT 421
Db 96884 ATGTTTGACCTATTAGCT 96904

RESULT 9
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LOCUS Rattus norvegicus clone CH230-362C16, *** SEQUENCING IN PROGRESS
DEFINITION *** 64 unordered pieces.
ACCESSION AC128082
VERSION AC128082.1 GI:21908679
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 178228)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-oshman, P.R., Allen, C.,
Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, K., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyne, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, B., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louseghed, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
Sodergren, E., Sonaika, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Taber, P., Tamerisa, K., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczky, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 178228)
Worley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

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COMMENT
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Baylor Plaza, Houston, TX 77030, USA
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Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information
Center project name: GZQW
Center clone name: CH230-362C16
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Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 116771 bases at least Q40
Consensus quality: 123909 bases at least Q30
Consensus quality: 129462 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 64 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1173: contig of 1173 bp in length
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6833: gap of unknown length
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8090: gap of unknown length
9641: contig of 1551 bp in length
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9742: contig of 1035 bp in length
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10877: contig of 1029 bp in length
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13321: gap of unknown length
13421: contig of 1258 bp in length
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22815: gap of unknown length
23949: contig of 1134 bp in length
24049: gap of unknown length
25331: contig of 1282 bp in length
25431: gap of unknown length
26617: contig of 1186 bp in length
26717: gap of unknown length
28435: contig of 1718 bp in length
28535: gap of unknown length
30650: contig of 2125 bp in length
30760: gap of unknown length
32263: contig of 1503 bp in length
32264: gap of unknown length
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32364
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34265: gap of unknown length
35302: contig of 1037 bp in length
35402: gap of unknown length
37282: contig of 1880 bp in length
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39160: contig of 1778 bp in length
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40880: contig of 1620 bp in length
40881: gap of unknown length
42436: contig of 1456 bp in length
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44381: contig of 1845 bp in length
44481: gap of unknown length
46391: contig of 1910 bp in length
46491: gap of unknown length
48409: contig of 1918 bp in length
48509: gap of unknown length
49931: contig of 1422 bp in length
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51371: contig of 1340 bp in length
51471: gap of unknown length
53362: contig of 1891 bp in length
53462: gap of unknown length
55170: contig of 1708 bp in length
55270: gap of unknown length
55371: contig of 1427 bp in length
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58037: contig of 1240 bp in length
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60361: contig of 2224 bp in length
60461: gap of unknown length
62335: contig of 1874 bp in length
62435: gap of unknown length
64906: contig of 2471 bp in length
65006: gap of unknown length
67475: contig of 2469 bp in length
67575: gap of unknown length
69553: contig of 2078 bp in length
69554: gap of unknown length
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73930: gap of unknown length
77047: contig of 3117 bp in length
77147: gap of unknown length
80438: contig of 3291 bp in length
80538: gap of unknown length
83532: contig of 2994 bp in length
83632: gap of unknown length
85754: contig of 2122 bp in length
85854: gap of unknown length
89203: contig of 3349 bp in length
89303: gap of unknown length
92865: contig of 3562 bp in length
92965: gap of unknown length
95863: gap of unknown length
95963: contig of 3835 bp in length
99798: gap of unknown length
99799: contig of 4554 bp in length
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104353: gap of unknown length
108165: contig of 3713 bp in length
108166: gap of unknown length
111945: contig of 3680 bp in length
112045: gap of unknown length
116301: contig of 4256 bp in length
116302: gap of unknown length
120825: contig of 4424 bp in length
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Best Local Similarity 100.0%; Score 21; DB 2; Length 178228;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      152  AAGCAAAAGCAGAGGGTGAAA 172
Db      33628 AAGCAAAAGCAGAGGGTGAAA 33648

RESULT 10
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DEFINITION Nostoc sp. PCC 7120 DNA, complete genome, section 7/19.
ACCESSION AP003587 BA000019
VERSION AP003587.1 GI:17130808
KEYWORDS
SOURCE Nostoc sp. PCC 7120 DNA.
ORGANISM Nostoc sp. PCC 7120
REFERENCE 1
AUTHORS Kaneko, T., Nakamura, Y., Wolk, C.P., Kuritz, T., Sasamoto, S.,
        Watanabe, A., Iriyuchi, M., Ishikawa, A., Kawashima, K., Kimura, T.,
        Kishida, Y., Kohara, M., Matsumoto, M., Matsuno, A., Muraki, A.,
        Nakazaki, N., Shimo, S., Sugimoto, M., Takazawa, M., Yamada, M.,
        Yasuda, M. and Tabata, S.
        Complete genomic sequence of the filamentous nitrogen-fixing
        cyanobacterium Anabaena sp. strain PCC 7120
        DNA Res. 8 (5), 205-213 (2001)
        21595285
        2 (bases 1 to 343550)
        Kaneko, T.
        Direct Submission
        Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
        Institute, The First Laboratory for Plant Gene Research, Yana
        1532-3, Kisarazu, Chiba 292-0812, Japan
        (E-mail: kaneko@kazusa.or.jp)
        URL: http://www.kazusa.or.jp/cyanobase/,
        Tel: 81-438-52-3935 (ex. 2338), Fax: 81-438-52-3934
        Location/Qualifiers
            1. 343550
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               /db_xref="taxon:103690"
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DFDNLNWEORSYAKWAGYDGLANLYFTYELDRKLKNGIDTTLTASHPGWTATLEQ
FTAGGIVKYLNGIVAQDITMGALPTLRAIEAGLGAEYFGPGFMEMEGYPIKVESN
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HITARDPETHFWNPGLKYECHIRVSDLVLVNRDGVVKGDALINQAFPAIHSI
EARPDVAAAHSAHSYGKAWSLGRLDPLTDACAFYEDHALLDDITGVVLETS
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LAGSOIOLKLEOSTVQGRSAVYRADYADYKVNRLKDIINNFFEIQPPNGYSLLSN
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TTIANPFGADFASGIVPKERKADRGSTQITWIFDDNVSVNPFQVFTNTNPIQTGII
PRLLLPALFLWILLYLSLPI SLTNVAIASSIYFACLLTLTLYLSRFMDAQLAWTM
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unknown protein
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gene
CDS
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AYDAGNSKNTINLEYLLANSPPORLLIFWDGASYHRSKEIRGFLDSVNSQSLPTEQWK
IHCVRPAPNCPVQNPTIEDIWLQAKTWRRFALIPSFHLKWFIFWFIHTTDFDTL
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DRISLGDQPFLEFVAVAPQPIITINQVAPLSAKHPFPPSPVFTQLFPIISIGKO
LTRKALVPGILTVFVFMFATVGPQANQIVATYIALAAYFYIRICGKPKPWV
LVGAALSTLILSLPLNLFIFIFREVLPGSPVPPDQVSSLTETLVFGVGLMEE
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LQAGTEVGLQVLTARILGLPAGHMYSGVLYGFIQAALKPRHAKOILAVGYLSAAL
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LHTAFTATGPQNMWIAATKAEIFASQSLGELQVCSVLPTWEADDLIFAPRY
AYSMRSEGNLTSTIVDNNVNSQWLSALSEVEQAKLSVAIYAIRQNDSPSES"
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Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 CCCAATGTTGCCAAATATGCT 363
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Db 36059 CCCAATGTTGCCAAATATGCT 36079

RESULT 11
HUMLDHX3

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LOCUS HUMLDHX3 188 bp DNA linear PRI 08-MAY-2000
DEFINITION Homo sapiens lactate dehydrogenase-C (LDHC) gene, exon 4.
ACCESSION M24512
VERSION M24512.1 GI:187069
KEYWORDS
SEGMENT 3 of 6
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 188)
AUTHORS Takano, T. and Li, S.S.
TITLE Human testicular lactate dehydrogenase-C gene is interrupted by six
introns at positions homologous to those of LDH-A (muscle) and
LDH-B (heart) genes
JOURNAL Biochem. Biophys. Res. Commun. 159 (2), 579-583 (1989)
MEDLINE 89193640
PUBMED 2930531
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by S.S.-L.Li, 28-APR-1989.
FEATURES
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1..188
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/db_xref="taxon:9606"
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/clone="hC[201,203,210,211,303]"
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<1..4
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179..>188
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGGTGATTC 566
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Db 154 ATTGGAGAACATGGTGATTC 173

RESULT 12
AF401096
LOCUS AF401096 811 bp mRNA linear PRI 02-AUG-2002
DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401096
VERSION AF401096.1 GI:22086508
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 811)
AUTHORS Koslowski, M., Tuercei, O. and Sahin, U.
TITLE Identification of new splice variants of testis-specific lactate
dehydrogenase C expressed exclusively in tumors by data-mining of
GenBank
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 811)
AUTHORS Koslowski, M., Tuercei, O. and Sahin, U.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2001) Department of Internal Medicine
III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
55131, Germany

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FEATURES
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      235 a 135 c 184 g 257 t
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      Best Local Similarity 2.1%; Score 20; DB 9; Length 811;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGGTGATTC 566
Db 508 ATTGGAGAACATGGTGATTC 527

RESULT 13
AF401095
LOCUS
DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401095
VERSION AF401095
KEYWORDS
SOURCE
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    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 879)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Identification of new splice variants of testis-specific lactate
    dehydrogenase C expressed exclusively in tumors by data-mining of
    GenBank
  JOURNAL
    Unpublished
    2 (bases 1 to 879)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Direct Submission
    Submitted (20-JUL-2001) Department of Internal Medicine
    III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
    55131, Germany
  FEATURES
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Qy 547 ATTGGAGAACATGGTGATTC 566
Db 334 ATTGGAGAACATGGTGATTC 353

RESULT 14
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LOCUS
DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401097
VERSION AF401097
KEYWORDS
SOURCE
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    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 1047)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Identification of new splice variants of testis-specific lactate
    dehydrogenase C expressed exclusively in tumors by data-mining of
    GenBank
  JOURNAL
    Unpublished
    2 (bases 1 to 1047)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Direct Submission
    Submitted (20-JUL-2001) Department of Internal Medicine
    III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
    55131, Germany
  FEATURES
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Db 626 ATTGGAGAACATGGTGATTC 645

RESULT 15
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DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401094
VERSION AF401094
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  REFERENCE
    1 (bases 1 to 1053)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Identification of new splice variants of testis-specific lactate
    dehydrogenase C expressed exclusively in tumors by data-mining of
    GenBank
  JOURNAL
    Unpublished
    2 (bases 1 to 1053)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Direct Submission
    Submitted (20-JUL-2001) Department of Internal Medicine
    III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
    55131, Germany
  FEATURES
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DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401097
VERSION AF401097
KEYWORDS
SOURCE
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  REFERENCE
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    Koslowski, M., Tuereci, O. and Sahin, U.
    Identification of new splice variants of testis-specific lactate
    dehydrogenase C expressed exclusively in tumors by data-mining of
    GenBank
  JOURNAL
    Unpublished
    2 (bases 1 to 1047)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Direct Submission
    Submitted (20-JUL-2001) Department of Internal Medicine
    III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
    55131, Germany
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          /note="lactate dehydrogenase C variant 6; tumor specific;
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      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGGTGATTC 566
Db 626 ATTGGAGAACATGGTGATTC 645

RESULT 15
AF401094
LOCUS
DEFINITION Homo sapiens lactate dehydrogenase C (LDHC) mRNA, complete
sequence, alternatively spliced.
ACCESSION AF401094
VERSION AF401094
KEYWORDS
SOURCE
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    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 1053)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Identification of new splice variants of testis-specific lactate
    dehydrogenase C expressed exclusively in tumors by data-mining of
    GenBank
  JOURNAL
    Unpublished
    2 (bases 1 to 1053)
    Koslowski, M., Tuereci, O. and Sahin, U.
    Direct Submission
    Submitted (20-JUL-2001) Department of Internal Medicine
    III/Hematology, University Mainz, Obere Zahlbacherstr. 63, Mainz
    55131, Germany
  FEATURES
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          /db_xref="taxon:9606"
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coding region not determined; lacks exon 3"
BASE COUNT 305 a 176 c 246 g 326 t
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy .547 ATGGAGAACATGGTGATTC 566
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Db 508 ATGGAGAACATGGTGATTC 527

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 10:16:32 ; Search time 278 Seconds
(without alignments)
7873.893 Million cell updates/sec

Title: US-09-992-430B-21

Perfect score: 972

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Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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21:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	2.1	1234	9	Sequence encoding
2	19	2.0	1680	24	Human cDNA encoding
3	19	2.0	1755	22	Human secreted pro
4	19	2.0	1759	22	Human secreted pro
5	19	2.0	4068	22	Mouse p97 (mp97) p
6	19	2.0	4158	22	DNA encoding membr
7	19	2.0	5313	23	Drosophila melanog
8	19	2.0	33140	22	Genomic fragment #
9	19	2.0	1082138	21	Arabidopsis thalia

Drosophila melanog
Fusarium venenatum
Bacillus clausii g
DNA encoding novel
Nucleotide sequenc
Arabidopsis thalia
Drosophila melanog
Drosophila melanog
Human nervous syst
Human nervous syst
Drosophila melanog
Human nervous syst
Drosophila melanog
Propionibacterium
Human nervous syst
Human nervous syst
Human immune/haema
Human nervous syst
Human immune/haema
Human nervous syst
Human immune/haema
Partial mouse WRN
L. lactis multiru
Haemophilus influe
Genomic sequence o
Genomic sequence o
Human foetal liver
Probe #19221 for g
Human brain expres
Human bone marrow
Probe #17829 for g
Probe #25565 used
Human genome-deriv
Tomato genomic DNA
Human ovarian PCR-
Human ovarian tumo
Pinus radiata xylo
S. cerevisiae YKRO
DNA encoding novel
Human ovarian tumo
Human ORFX polynuc
Human foetal liver
Probe #9660 for ge
Human brain expres
Human bone marrow
Probe #8956 for ge
Probe #12851 used
Human genome-deriv
C. glutamicum SRT
DNA encoding novel
Human breast cance
Human breast cance
DNA encoding novel
Arabidopsis thalia
Arabidopsis thalia
Soybean branched c
S. epidermidis ope
S. epidermidis ope
Staphylococcus epi
cDNA encoding chic
Arabidopsis thalia
Human immune/haema
Arabidopsis thalia
Plasmodium falcipa
ced-9 coding seque
Drosophila melanog
C glutamicum codin
Streptococcus pneu
S. pneumoniae SP00
HPV type 18 Li gen
Soybean sulphite o
Human papillomavir
Drosophila melanog
Human cDNA sequenc

c 83	17	1.7	1884	22	AAH64742	Human secreted pro	c 156	16	1.6	176	23	ABV38418	Human prostate exp
c 84	17	1.7	1954	22	AAH20950	Wheat arginyl-tRNA	c 157	16	1.6	233	21	AAC21576	Human secreted pro
c 85	17	1.7	1992	24	AAQ23809	Rat sequence diffe	c 158	16	1.6	240	22	AAK23943	Human brain expres
c 86	17	1.7	2387	14	AAQ48438	Brh-1 CDNA, Braco	c 159	16	1.6	240	24	ABN66494	Streptococcus poly
c 87	17	1.7	2387	17	AAT45675	Wasp Brh-1 toxin g	c 160	16	1.6	251	19	AAH11049	Human biallelic po
c 88	17	1.7	2387	22	AAS05984	Parasitic wasp ins	c 161	16	1.6	251	19	AAH11050	Human biallelic po
c 89	17	1.7	2642	23	ABL10304	Drosophila melanog	c 162	16	1.6	261	14	AAQ39685	Expressed Sequence
c 90	17	1.7	3019	22	AAH54991	S. epidermidis gen	c 163	16	1.6	289	21	AAQ49263	Human hydrolase ho
c 91	17	1.7	3172	21	AAH5794	Apoptosis related	c 164	16	1.6	289	21	AAZ49263	Antisense DNA comp
c 92	17	1.7	3532	22	AAH15730	Human CDNA sequenc	c 165	16	1.6	300	13	AAQ25393	RI alpha 100 N-ter
c 93	17	1.7	3573	23	ABL05120	Drosophila melanog	c 166	16	1.6	300	17	AAQ25394	A fragment of the
c 94	17	1.7	3799	24	ABK70290	Human lung cancer	c 167	16	1.6	300	17	AAH34984	A fragment of the
c 95	17	1.7	3799	24	ABK24337	DNA encoding human	c 168	16	1.6	300	18	AAH34989	RI-alpha antisense
c 96	17	1.7	4082	22	ABK09788	Human ovarian tumo	c 169	16	1.6	300	18	AAH77365	RI-alpha 5'-termin
c 97	17	1.7	4093	22	AAH54429	S. epidermidis gen	c 170	16	1.6	300	21	AAZ59438	CAMP dependent kin
c 98	17	1.7	4239	23	AAS64518	DNA encoding novel	c 171	16	1.6	300	21	AAZ59439	CAMP dependent kin
c 99	17	1.7	4715	22	AAH84674	Human immune/haema	c 172	16	1.6	310	22	AAK76777	Human immune/haema
c 100	17	1.7	4881	19	AAV52258	Streptococcus pneu	c 173	16	1.6	316	20	AAZ21544	Fragment of progre
c 101	17	1.7	4902	23	AAS85161	DNA encoding novel	c 174	16	1.6	316	20	AAZ21544	Clone PEGen-28 seq
c 102	17	1.7	5107	24	AAS85161	Human immune syste	c 175	16	1.6	321	21	AAH39327	S. lactificifex 16S
c 103	17	1.7	5279	23	AAS85168	DNA encoding novel	c 176	16	1.6	324	24	AAH39327	DLF10-1 adenylate
c 104	17	1.7	5326	23	ABL29084	Drosophila melanog	c 177	16	1.6	326	24	ABQ55704	Human ovarian anti
c 105	17	1.7	5600	13	AAQ21678	pHCV-31 - recombin	c 178	16	1.6	328	23	ABQ55704	Human prostate exp
c 106	17	1.7	5600	13	AAQ22963	Sequence of pHCV-3	c 179	16	1.6	340	22	AAH86119	Human polynucleoti
c 107	17	1.7	5600	14	AAQ38266	HCV CKS-33-BCD fus	c 180	16	1.6	345	24	ABL62008	Colon adenocarcino
c 108	17	1.7	5600	14	AAQ38251	HCV CKS-33-BCD fus	c 181	16	1.6	345	24	ABL62008	Colon adenocarcino
c 109	17	1.7	5600	14	AAQ38251	HCV CKS-33-BCD fus	c 182	16	1.6	354	21	AAH56838	Pinus radiata tran
c 110	17	1.7	5600	15	AAQ62663	pHCV-31 plasmid ex	c 183	16	1.6	369	22	AAH56838	Human polynucleoti
c 111	17	1.7	6046	22	AAH32219	HCV recombinant an	c 184	16	1.6	426	22	AAH34655	Human colon cancer
c 112	17	1.7	6046	23	ABL07762	Drosophila melanog	c 185	16	1.6	435	22	AAH30998	Human diagnostic a
c 113	17	1.7	6560	15	AAQ54629	Genomic region con	c 186	16	1.6	438	21	AAH30998	Cat flea hindgut a
c 114	17	1.7	6765	22	AAH90108	Human bone marrow	c 187	16	1.6	438	21	AAH90494	M. capusculatus gene
c 115	17	1.7	6798	22	AAH39051	Human excretory re	c 188	16	1.6	448	21	AAH90494	Pinus radiata tran
c 116	17	1.7	6798	22	AAH39051	Human kidney relat	c 189	16	1.6	450	20	AAH90494	Human prostate can
c 117	17	1.7	6798	23	ABK44028	Genomic DNA encodi	c 190	16	1.6	452	20	AAH90494	EST clone GY520
c 118	17	1.7	7491	24	ABL33585	Human immune syste	c 191	16	1.6	462	22	ABA46157	Human breast cell
c 119	17	1.7	7536	23	ABL08520	Drosophila melanog	c 192	16	1.6	462	22	AAK30360	Human bone marrow
c 120	17	1.7	8022	18	AAH61982	Yeast rad3 gene.	c 193	16	1.6	462	22	AAH61982	Probe #4729 used t
c 121	17	1.7	9001	22	AAH61982	Human immune/haema	c 194	16	1.6	462	22	AAH61982	Human genome-deriv
c 122	17	1.7	9179	23	ABL03688	Drosophila melanog	c 195	16	1.6	464	21	AAA42393	Human secreted exp
c 123	17	1.7	9771	22	AAH71552	Human immune/haema	c 196	16	1.6	465	22	AAH98232	Human EST-derived
c 124	17	1.7	9979	22	AAH81194	Human immune/haema	c 197	16	1.6	477	23	ABV61300	Human prostate exp
c 125	17	1.7	10382	22	AAH74784	Human immune/haema	c 198	16	1.6	477	23	AAH85093	DNA encoding novel
c 126	17	1.7	12177	23	ABL03724	Drosophila melanog	c 199	16	1.6	484	22	AAH93377	Spinal cord tissue
c 127	17	1.7	13673	22	AAH76548	Human immune/haema	c 200	16	1.6	495	22	AAH40318	DNA encoding human
c 128	17	1.7	13673	22	AAH81195	Human immune/haema	c 201	16	1.6	495	22	AAH40318	Human reproductive
c 129	17	1.7	14676	22	AAH71553	Human immune/haema	c 202	16	1.6	504	23	ABV61372	Human prostate exp
c 130	17	1.7	15496	22	AAH71549	Human lung antigen	c 203	16	1.6	508	21	AAH07611	Human secreted pro
c 131	17	1.7	16766	24	ABL34157	Human immune syste	c 204	16	1.6	514	22	AAH07611	Human cDNA clone (
c 132	17	1.7	16766	22	AAH85126	Human immune/haema	c 205	16	1.6	524	24	ABQ51908	Oligonucleotide fo
c 133	17	1.7	16983	22	AAH85126	Human immune/haema	c 206	16	1.6	524	24	ABQ51909	Oligonucleotide fo
c 134	17	1.7	19191	22	AAH67485	Human immune/haema	c 207	16	1.6	528	15	AAH73887	Borrelia 297 anti
c 135	17	1.7	21724	22	AAH26629	Human genomic DNA	c 208	16	1.6	535	23	ABV51010	Human prostate exp
c 136	17	1.7	21724	22	AAH86125	Human immune/haema	c 209	16	1.6	535	24	ABQ34610	Oligonucleotide fo
c 137	17	1.7	21727	22	AAH26630	Human immune/haema	c 210	16	1.6	553	24	ABQ34611	Oligonucleotide fo
c 138	17	1.7	21727	22	AAH86126	Human immune/haema	c 211	16	1.6	554	22	AAH11282	Oligonucleotide fo
c 139	17	1.7	23054	22	AAH84676	Human immune/haema	c 212	16	1.6	563	24	AAH62146	Human cancer relat
c 140	17	1.7	32217	22	AAH91742	Genomic sequence #	c 213	16	1.6	573	22	AAH29011	Burgdorferi ospc
c 141	17	1.7	34488	22	AAH91742	Human neuroblastom	c 214	16	1.6	579	15	AAH73887	Borrelia 297 anti
c 142	17	1.7	50925	21	AAH81487	N. meningitidis pa	c 215	16	1.6	579	21	AAH39326	S. lactificifex 16S
c 143	17	1.7	59560	22	AAH71550	Human immune/haema	c 216	16	1.6	580	22	AAH02557	Human reproductive
c 144	17	1.7	59560	22	AAH80620	Human immune/haema	c 217	16	1.6	595	22	AAH61803	Human immune/haema
c 145	17	1.7	114793	22	AAH08215	Human genome from	c 218	16	1.6	595	22	AAH34776	CDNA encoding nove
c 146	17	1.7	121162	21	AAH66548	Human kinesin-like	c 219	16	1.6	615	21	AAH49233	Human hydrolase ho
c 147	17	1.7	128600	24	AAH83461	Human CDNA differe	c 220	16	1.6	621	22	AAH45236	CDNA encoding nove
c 148	17	1.7	309400	22	AAH68534	C glutamicum codin	c 221	16	1.6	623	22	AAH45048	CDNA encoding nove
c 149	17	1.7	349980	21	AAH21610	Neisseria meningit	c 222	16	1.6	645	22	AAH40380	DNA encoding human
c 150	17	1.7	534720	19	AAH30458	Rhizobium species	c 223	16	1.6	645	22	AAH40380	DNA encoding human
c 151	17	1.7	536165	19	AAH30459	Rhizobium species	c 224	16	1.6	645	22	AAH40380	Human reproductive
c 152	17	1.7	1230025	20	AAH31990	Nucleotide sequenc	c 225	16	1.6	645	22	AAH40380	Human reproductive
c 153	17	1.7	1437668	21	AAH81490	N. meningitidis B	c 226	16	1.6	663	11	AAH05615	Insert from pARC 1
c 154	16	1.6	81	18	AAH57932	L-selectin orphan	c 227	16	1.6	694	21	AAH253850	Neisseria gonorrhoe
c 155	16	1.6	87	16	AAH19428	Human gene signatu	c 228	16	1.6	700	22	AAH92618	Human inflammatory

c 229	16	1.6	708	24	ABQ37310	Oligonucleotide fo	c 302	16	1.6	1538	20	AAZ21530	Progression elevat
c 230	16	1.6	708	24	ABQ37311	Oligonucleotide fo	c 303	16	1.6	1544	18	ABN86839	cDNA encoding rat
c 231	16	1.6	738	22	AAH05900	Human cDNA clone (c 304	16	1.6	1573	24	ARN86082	Human caudal actio
c 232	16	1.6	744	21	AAZ53851	Neisseria meningit	c 305	16	1.6	1588	24	ABQ54276	Human ovarian anti
c 233	16	1.6	749	22	AAI95692	Human neuroblastom	c 306	16	1.6	1614	22	ABQ98192	Human EST-derived
c 234	16	1.6	761	22	AAI96716	Human neuroblastom	c 307	16	1.6	1632	23	ABV24429	Human prostate exp
c 235	16	1.6	762	24	ABQ68999	Listeria monocytog	c 308	16	1.6	1668	22	AAH43384	cDNA sequence enco
c 236	16	1.6	812	21	AAZ35438	Arabidopsis thalia	c 309	16	1.6	1683	23	AAZ54012	Klebsiella pneumon
c 237	16	1.6	812	24	ABQ35900	Oligonucleotide fo	c 310	16	1.6	1688	22	AAK68785	Human immune/haema
c 238	16	1.6	812	24	ABQ35901	Oligonucleotide fo	c 311	16	1.6	1709	13	AAQ29277	Encodes secreted f
c 239	16	1.6	815	21	AAZ39440	Arabidopsis thalia	c 312	16	1.6	1714	21	AAZ93536	Cat flea HMT Na/K
c 240	16	1.6	825	22	AAH65959	C glutamic codin	c 313	16	1.6	1714	21	AAZ93537	Cat flea HMT Na/K
c 241	16	1.6	829	20	AAZ13623	Enterococcus faeca	c 314	16	1.6	1737	19	AAV29053	Alcohol and/or ald
c 242	16	1.6	873	23	AAZ87910	DNA encoding novel	c 315	16	1.6	1741	22	AAK56769	Human immune/haema
c 243	16	1.6	879	22	AAF27597	Mevalonate pathway	c 316	16	1.6	1750	22	AAH14806	Human cDNA sequenc
c 244	16	1.6	891	24	ABN69039	Streptococcus poly	c 317	16	1.6	1751	24	ABL90377	Human polynucleoti
c 245	16	1.6	895	23	ABV25466	Human prostate exp	c 318	16	1.6	1785	19	AAV41902	Nucleotide sequenc
c 246	16	1.6	941	24	ABK12491	Arabidopsis thalia	c 319	16	1.6	1788	23	AAZ51607	Staphylococcus aur
c 247	16	1.6	960	19	AAV53346	DNA encoding a Sta	c 320	16	1.6	1806	19	AAV41901	Nucleotide sequenc
c 248	16	1.6	972	23	ABL22115	Drosophila melanog	c 321	16	1.6	1815	23	AAZ54790	Staphylococcus aur
c 249	16	1.6	978	21	AAZ93338	Cat flea HMT Na/K	c 322	16	1.6	1828	23	ABL20439	Drosophila melanog
c 250	16	1.6	978	21	AAZ93339	Cat flea HMT Na/K	c 323	16	1.6	1854	22	AAI59167	Human polynucleoti
c 251	16	1.6	987	23	AAZ56137	Salmonella typhi D	c 324	16	1.6	1848	21	AAZ81726	Human secreted pro
c 252	16	1.6	1001	21	AAZ57469	Arachidonic acid m	c 325	16	1.6	1949	22	AAH75170	Nucleotide sequenc
c 253	16	1.6	1023	23	ABL27951	Drosophila melanog	c 326	16	1.6	1967	22	ABA44267	Human breast cell
c 254	16	1.6	1036	21	AAZ16278	Human prostate can	c 327	16	1.6	1967	22	ABA54718	Human foetal liver
c 255	16	1.6	1066	21	AAA26671	Candida albicans p	c 328	16	1.6	1967	22	ABA24498	Probe #2964 for ge
c 256	16	1.6	1066	22	AAZ76852	Human secreted pro	c 329	16	1.6	1967	22	AAK03000	Human brain expres
c 257	16	1.6	1068	24	ABK73448	Bacillus lichenifo	c 330	16	1.6	1967	22	AAZ28450	Human bone marrow
c 258	16	1.6	1084	22	AAI61153	Human polynucleoti	c 331	16	1.6	1967	22	AAI13018	Probe #2951 for ge
c 259	16	1.6	1089	24	ABN70774	Streptococcus poly	c 332	16	1.6	1967	22	AAI34371	Probe #3057 used t
c 260	16	1.6	1107	22	AAZ29022	Borrelia sp chimer	c 333	16	1.6	1967	22	AAI02933	Probe #2924 used t
c 261	16	1.6	1110	22	AAZ27709	Human transport pr	c 334	16	1.6	1967	22	AAZ00836	Human cDNA clone H
c 262	16	1.6	1113	22	AAZ29019	Borrelia sp chimer	c 335	16	1.6	1967	24	ABS02957	Human genome-deriv
c 263	16	1.6	1121	21	AAZ89015	A. ambisexualis Aa	c 336	16	1.6	1982	23	ABL27901	Drosophila melanog
c 264	16	1.6	1125	24	ABN66495	Streptococcus poly	c 337	16	1.6	1997	24	ABI99512	Mouse ischaemic co
c 265	16	1.6	1128	22	AAZ29014	Borrelia sp chimer	c 338	16	1.6	2025	22	AAI92899	Human polynucleoti
c 266	16	1.6	1137	22	AAZ29016	Borrelia sp chimer	c 339	16	1.6	2054	13	AAQ02462	Aspergillus tubige
c 267	16	1.6	1176	24	ABL39743	Human NS cDNA sequ	c 340	16	1.6	2054	22	AAZ00973	Sequence of human
c 268	16	1.6	1179	22	AAZ29038	Borrelia sp chimer	c 341	16	1.6	2095	8	AAZ70692	Atrial natriuretic
c 269	16	1.6	1195	22	AAZ29034	Borrelia sp chimer	c 342	16	1.6	2095	17	AAZ27029	Arabidopsis thalia
c 270	16	1.6	1196	21	AAZ53987	Arabidopsis thalia	c 343	16	1.6	2096	21	AAZ50354	Human secreted pro
c 271	16	1.6	1197	22	AAZ29032	Borrelia sp chimer	c 344	16	1.6	2102	22	AAZ33214	C. albicans FKSI h
c 272	16	1.6	1209	22	AAZ29042	Borrelia sp chimer	c 345	16	1.6	2129	16	AAQ86899	Human digestive sy
c 273	16	1.6	1239	23	AAZ54243	Pseudomonas aerugi	c 346	16	1.6	2147	22	AAZ91479	Human colorectal c
c 274	16	1.6	1267	23	ABL21425	Drosophila melanog	c 347	16	1.6	2147	22	AAI57789	DNA encoding novel
c 275	16	1.6	1277	21	AAZ40265	Arabidopsis thalia	c 348	16	1.6	2187	23	AAZ53444	DNA encoding novel
c 276	16	1.6	1277	21	AAZ40801	Arabidopsis thalia	c 349	16	1.6	2187	23	AAZ71960	DNA encoding novel
c 277	16	1.6	1292	22	AAZ90003	Nucleotide sequenc	c 350	16	1.6	2187	23	AAZ82384	DNA encoding novel
c 278	16	1.6	1299	24	ABK73383	Bacillus lichenifo	c 351	16	1.6	2187	23	AAZ90134	DNA encoding novel
c 279	16	1.6	1316	24	ABQ65390	Human cyplai gene	c 352	16	1.6	2187	23	AAZ90134	Human ovarian and
c 280	16	1.6	1331	13	AAZ24681	H23-ETA-S antigen	c 353	16	1.6	2236	22	ABA07878	Human reproductive
c 281	16	1.6	1345	22	ABA49421	Human breast cell	c 354	16	1.6	2236	22	AAZ03695	Human immune/haema
c 282	16	1.6	1345	22	ABA67334	Human foetal liver	c 355	16	1.6	2236	22	AAK66847	Human immune/haema
c 283	16	1.6	1345	22	ABA34425	Probe #12891 for g	c 356	16	1.6	2236	22	AAK69056	Human immune/haema
c 284	16	1.6	1345	22	AAK15766	Human brain expres	c 357	16	1.6	2236	22	AAK72813	Human immune/haema
c 285	16	1.6	1345	22	AAK41508	Human bone marrow	c 358	16	1.6	2260	21	AAZ48244	Human oxidoreducta
c 286	16	1.6	1345	22	AAI22256	Probe #12189 for g	c 359	16	1.6	2260	21	AAZ48244	Human hydrolase ho
c 287	16	1.6	1345	22	AAI47547	Probe #16233 used	c 360	16	1.6	2266	22	AAZ52838	Human cDNA encodin
c 288	16	1.6	1345	22	AAI07952	Probe #7943 used t	c 361	16	1.6	2268	23	AAZ52421	Human DNA encodin
c 289	16	1.6	1345	24	ABZ15512	Human genome-deriv	c 362	16	1.6	2292	24	ABQ70772	E. coli DNA for ce
c 290	16	1.6	1350	23	AAZ89168	DNA encoding novel	c 363	16	1.6	2310	24	AAZ94752	Listeria monocytog
c 291	16	1.6	1412	21	AAZ76222	Human ORFX ORF177	c 364	16	1.6	2394	22	AAZ85095	Human DNA sequenc
c 292	16	1.6	1475	9	AAZ80638	Sequence of cDNA e	c 365	16	1.6	2417	22	AAH14267	Atherosclerosis-as
c 293	16	1.6	1483	24	ABL90081	Human polynucleoti	c 366	16	1.6	2471	24	AAI72320	Human cDNA sequenc
c 294	16	1.6	1484	22	AAZ27394	cDNA encoding nove	c 367	16	1.6	2490	23	AAZ86902	DNA encoding novel
c 295	16	1.6	1484	23	ABK43598	DNA encoding novel	c 368	16	1.6	2513	22	AAK64965	Human immune/haema
c 296	16	1.6	1491	24	ABN91403	Staphylococcus epi	c 369	16	1.6	2520	14	AAQ40580	Glutaryl-7-amino c
c 297	16	1.6	1521	24	ABN81317	Arabidopsis thalia	c 370	16	1.6	2550	23	ABL20341	Drosophila melanog
c 298	16	1.6	1524	23	AAZ575643	DNA encoding novel	c 371	16	1.6	2580	22	AAH54959	S. epidermidis gen
c 299	16	1.6	1524	23	AAZ83665	DNA encoding novel	c 372	16	1.6	2591	22	AAH18566	Human cDNA sequenc
c 300	16	1.6	1534	21	AAZ33954	Arabidopsis thalia	c 373	16	1.6	2619	21	AAZ77768	Human cancer assoc
c 301	16	1.6	1536	24	ABK84287	Human cDNA differe	c 374	16	1.6	2655	23	AAZ71962	DNA encoding novel

375	16	1.6	2655	23	AAS72667	DNA encoding novel	448	16	1.6	6746	23	ABL14122	Drosophila melanog
376	16	1.6	2655	23	AAS77516	DNA encoding novel	449	16	1.6	6891	23	AAS85215	DNA encoding novel
377	16	1.6	2655	23	AAS80016	DNA encoding novel	450	16	1.6	6920	23	AAS98318	Chicken EST-derive
378	16	1.6	2668	23	ABL09903	Drosophila melanog	451	16	1.6	7032	22	AAS85436	DNA encoding novel
379	16	1.6	2682	22	ABK83742	Human cDNA differe	452	16	1.6	7033	22	AAS46522	Tumour suppressor
380	16	1.6	2702	22	AAS60836	Human cancer agent	453	16	1.6	8178	24	ABL32087	Human immune syste
381	16	1.6	2702	22	AAS60840	Human cancer agent	454	16	1.6	8181	24	ABL41001	Human neuregulin 2
382	16	1.6	2795	23	ABL16644	Drosophila melanog	455	16	1.6	8342	24	ABL32500	Human immune syste
383	16	1.6	2853	22	AAS33096	Human secreted pro	456	16	1.6	8473	20	AXA25487	Human myosin IXa c
384	16	1.6	2856	22	AAS44076	S. epidermidis gen	457	16	1.6	8483	23	ABL25370	Drosophila melanog
385	16	1.6	2926	23	ABL14123	Drosophila melanog	458	16	1.6	9164	20	AXA82259	Beta-domain delete
386	16	1.6	2982	22	AAS45191	S. epidermidis gen	459	16	1.6	9496	22	ABA16328	Human nervous syst
387	16	1.6	2991	19	AAS52588	Vascular endotheli	460	16	1.6	10455	20	AXA02095	Glycine max protop
388	16	1.6	2994	23	AAS85147	DNA encoding novel	461	16	1.6	10598	22	ABL27241	Drosophila melanog
389	16	1.6	3023	23	ABL7950	Drosophila melanog	462	16	1.6	10829	22	AXA28279	Nucleotide sequenc
390	16	1.6	3036	24	ABK84001	Human cDNA differe	463	16	1.6	10856	24	ABL32457	Human immune syste
391	16	1.6	3102	21	AAC75441	Human ORFX ORF996	464	16	1.6	10966	22	AAF32380	Hordeum vulgare L.
392	16	1.6	3133	22	AAS14528	Human cDNA sequenc	465	16	1.6	11846	20	AXA82261	Factor VIII protei
393	16	1.6	3227	22	AAS45410	S. epidermidis gen	466	16	1.6	12010	23	ABL06138	Drosophila melanog
394	16	1.6	3267	22	AAS45413	Human polynucleoti	467	16	1.6	12022	20	AXA82260	Factor VIII protei
395	16	1.6	3377	22	AAF72801	Secreted protein g	468	16	1.6	13525	23	ABL27900	Drosophila melanog
396	16	1.6	3377	22	AAF72828	Secreted protein g	469	16	1.6	14063	22	AXA82933	Human immune/haema
397	16	1.6	3382	23	ABL22114	Drosophila melanog	470	16	1.6	14063	22	AXA82934	Human immune/haema
398	16	1.6	3429	22	ABA08830	Human protein kina	471	16	1.6	15231	24	ABK63598	Rat sequence diffe
399	16	1.6	3465	23	ABL20199	Drosophila melanog	472	16	1.6	15366	22	AAS28623	Genomic sequence #
400	16	1.6	3503	23	ABL25371	Drosophila melanog	473	16	1.6	15667	22	ABL27240	Drosophila melanog
401	16	1.6	3636	23	ABL11340	Drosophila melanog	474	16	1.6	16750	22	AAS46314	Tumour suppressor
402	16	1.6	3825	23	ABV25634	Human prostate exp	475	16	1.6	16750	24	ABL32521	Human immune syste
403	16	1.6	3900	23	AAS64300	DNA encoding novel	476	16	1.6	16857	23	ABL28687	Drosophila melanog
404	16	1.6	4002	22	AAS15583	Human cDNA sequenc	477	16	1.6	17687	22	AAK64966	Human immune/haema
405	16	1.6	4024	23	ABL15060	Drosophila melanog	478	16	1.6	17687	22	AAK71665	Human immune/haema
406	16	1.6	4154	22	ADJ12785	Human nuclear horm	479	16	1.6	17689	23	ABL06316	Drosophila melanog
407	16	1.6	4207	22	ABA17738	Human nervous syst	480	16	1.6	17959	24	ABL54342	Chemically treated
408	16	1.6	4208	22	ABA17739	Human nervous syst	481	16	1.6	17959	24	ABL32575	Human immune syste
409	16	1.6	4208	22	ABA17739	Human nervous syst	482	16	1.6	17979	22	AAK6103	Human immune/haema
410	16	1.6	4230	23	AAS76399	DNA encoding novel	483	16	1.6	17979	22	AAK71664	Drosophila melanog
411	16	1.6	4231	23	ABL22756	Drosophila melanog	484	16	1.6	18439	23	ABL17911	Human immune/haema
412	16	1.6	4270	22	AAS43377	DNA sequence encod	485	16	1.6	18449	22	ABA20913	Human nervous syst
413	16	1.6	4287	24	ABN79843	Fungal ZBC gene se	486	16	1.6	18449	22	AAK27797	DNA encoding novel
414	16	1.6	4299	24	ABN79813	Fungal ZBC gene se	487	16	1.6	19209	22	AAK70154	Human immune/haema
415	16	1.6	4341	23	ABL20396	Drosophila melanog	488	16	1.6	19209	22	AAK6103	Human immune/haema
416	16	1.6	4607	24	ABK46540	DNA encoding human	489	16	1.6	20284	21	AAK69139	Human ABC1 gene ex
417	16	1.6	4620	23	AAS85216	DNA encoding novel	490	16	1.6	20829	23	ABL14502	Drosophila melanog
418	16	1.6	4679	22	AAF75865	Histidine protein k	491	16	1.6	21382	23	AAS59557	Propionibacterium
419	16	1.6	4711	21	AAC76508	Human ORFX ORP2063	492	16	1.6	21423	22	ABL36470	Human musculoskele
420	16	1.6	4715	22	AAS99638	Human protein enco	493	16	1.6	21423	22	ABL06154	Drosophila melanog
421	16	1.6	4722	23	ABL21424	Drosophila melanog	494	16	1.6	22081	22	AAF97862	Human neuroblastom
422	16	1.6	4858	23	ABL20437	Drosophila melanog	495	16	1.6	27423	23	ABL04268	Drosophila melanog
423	16	1.6	4972	23	ABL20340	Drosophila melanog	496	16	1.6	31208	24	ABK52899	Genomic DNA encodi
424	16	1.6	4989	23	ABL09902	Drosophila melanog	497	16	1.6	32190	22	AAS29937	Human lung antigen
425	16	1.6	5004	23	ABL18692	Drosophila melanog	498	16	1.6	32190	22	AAK89689	Human digestive sy
426	16	1.6	5145	19	AAV45185	Nucleotide sequenc	499	16	1.6	32193	22	AAS29936	Human lung antigen
427	16	1.6	5203	22	AAS46473	Tumour suppressor	500	16	1.6	32249	22	AAS29938	Chemically treated
428	16	1.6	5203	22	ABN80188	Human chemically m	501	16	1.6	34548	24	ABL70603	Human lung antigen
429	16	1.6	5311	22	ABA21074	Human nervous syst	502	16	1.6	40766	23	ABL28686	Chemically treated
430	16	1.6	5311	22	AAJ07486	Human reproductive	503	16	1.6	42429	23	ABL17910	Drosophila melanog
431	16	1.6	5339	24	ABA97074	Human fank cDNA.	504	16	1.6	43058	24	ABN97455	Drosophila melanog
432	16	1.6	5465	23	ABL20198	Drosophila melanog	505	16	1.6	43058	24	ABL64982	Gene #3953 used to
433	16	1.6	5694	22	AAS23416	Candida albicans e	506	16	1.6	43058	24	ABL65219	Lung cancer relate
434	16	1.6	5774	22	AAS46652	Tumour suppressor	507	16	1.6	49767	21	AAA81458	Lung cancer relate
435	16	1.6	5774	24	ABL33163	Human immune syste	508	16	1.6	49999	24	ABQ09884	N. meningitidis pa
436	16	1.6	5788	24	ABK39942	Human chemically p	509	16	1.6	55795	24	ABN95045	M. capulatus gene
437	16	1.6	5874	23	AAS85420	DNA encoding novel	510	16	1.6	55795	24	ABL68242	Gene #1543 used to
438	16	1.6	6160	24	ABL70233	Chemically treated	511	16	1.6	55795	24	ABL68484	Kidney cancer rela
439	16	1.6	6160	24	ABK31272	Signal transductio	512	16	1.6	55795	24	ABL68863	Kidney cancer rela
440	16	1.6	6228	23	ABL11144	Drosophila melanog	513	16	1.6	58407	19	AAV21210	Methanococcus jann
441	16	1.6	6286	24	ABL60158	Human MUC1 encodin	514	16	1.6	112190	22	AAH44801	BAC containing rep
442	16	1.6	6363	23	ABL16645	Drosophila melanog	515	16	1.6	129021	21	AAF22296	HAC adenocarcino
443	16	1.6	6394	24	AAS61278	Human gene regulat	516	16	1.6	145831	24	ABL62309	Lung cancer relate
444	16	1.6	6394	24	ABK31374	Signal transductio	517	16	1.6	145831	24	ABL68806	Lung cancer relate
445	16	1.6	6651	24	ABL61742	Colon adenocarcino	518	16	1.6	145831	24	ABL68888	Kidney cancer rela
446	16	1.6	6651	24	ABL64868	Lung cancer relate	519	16	1.6	145831	24	ABL69213	Prostate cancer re
447	16	1.6	6651	24	ABL65907	Lung cancer relate	520	16	1.6	147419	24	ABK83574	Human cDNA differe

521	16	1.6	172325	21	AAF21613	Neisseria meningit	594	15	340	23	ABV16598	Human prostate exp
c 522	16	1.6	183999	22	AAF92831	Human ABC1 genomic	595	15	345	20	AA334718	C. albicans antipeptide
c 523	16	1.6	349980	22	AAH68526	C Glutamicum codin	c 596	15	345	20	ABL98864	O. cuniculi concptide
c 524	16	1.6	349980	22	AAH68527	C Glutamicum codin	597	15	351	20	AA384223	DNA encoding human
525	16	1.6	349980	22	AAH68532	C Glutamicum codin	598	15	351	21	AA379452	Known human breast
526	16	1.6	684707	24	ABQ67196	Listeria innocua c	599	15	351	21	ABK76469	Bacillus lichenifo
527	16	1.6	837096	21	AAAB1489	N. meningitidis pa	600	15	351	24	ABK28996	Human breast tumou
528	16	1.6	910715	20	AA202488	Borrelia burgdorfe	c 601	15	352	24	ABL62601	Colon adenocarcino
529	16	1.6	1503900	22	AAK95240	Human neuroregulin-1	602	15	353	16	AAT35122	Enhanced expressio
530	16	1.6	1503900	22	AAK95243	Human neuroregulin-1	c 603	15	354	22	AAH67708	C glutamicum codin
c 531	16	1.6	1664976	19	AAV211209	Methanococcus jann	604	15	356	23	ABV47189	Human prostate exp
c 532	16	1.6	1664976	19	AAV211209	Methanococcus jann	605	15	356	23	ABV53622	Human prostate exp
c 533	16	1.6	2155561	24	AAH71527	Streptococcus poly	606	15	357	22	AAK59341	Human immune/haema
c 534	16	1.6	3011208	24	ABQ69245	Listeria innocua D	c 607	15	357	23	ABV52080	Human prostate exp
c 535	16	1.6	4403765	22	AA199683	Mycobacterium tube	608	15	363	24	ABK44171	CDNA #111 encoding
c 536	16	1.6	4411529	22	AA199682	Mycobacterium tube	c 609	15	363	24	ABK44172	CDNA #112 encoding
c 537	15	1.5	24	AAH75007	PCR primer for hum	610	15	363	24	AAH24872	Rat fibulin-1D DNA	
c 538	15	1.5	45	AAV65907	Probe oligonucleot	611	15	369	22	AAK56802	Human immune/haema	
c 539	15	1.5	50	AAH94541	NDV fusion protein	612	15	369	22	AAK56802	DNA encoding nove	
540	15	1.5	60	AAH38727	Human spliced tran	c 613	15	373	23	AA590123	Human ovarian can	
541	15	1.5	60	AAH48086	Human spliced tran	614	15	373	24	ABL79217	Human breast cance	
c 542	15	1.5	65	AAH27492	Rat spliced trans	615	15	375	22	AAH22740	Human breast cance	
543	15	1.5	80	AAV57946	708 vkcea primary	616	15	375	24	ABK44097	CDNA #37 encoding	
544	15	1.5	80	AAV57936	708 vk primary rea	c 617	15	375	24	ABK44176	CDNA #116 encoding	
545	15	1.5	80	AAV81078	Vaccine 1 708 VL c	618	15	375	24	ABK44177	CDNA #117 encoding	
546	15	1.5	80	AAV81099	Vaccine 2 708 VL c	c 619	15	375	24	ABK44188	CDNA #128 encoding	
547	15	1.5	80	AAV81055	De-immunised 708 V	c 620	15	375	24	ABK44189	CDNA #129 encoding	
548	15	1.5	106	AAH64922	Human cancer relat	c 621	15	377	24	ABL64922	Lung cancer relate	
549	15	1.5	148	AAH06506	Human secreted pro	c 622	15	378	24	ABN18964	Human ORFX polynuc	
c 550	15	1.5	155	AAH35537	Human musculoskele	c 623	15	384	19	AAH44195	Lettuce resistance	
c 551	15	1.5	173	AAH68568	Human lung tumour	c 624	15	384	24	ABK67792	Lettuce pest resis	
c 552	15	1.5	173	AAH38479	CDNA encoding clon	c 625	15	386	22	AAH13287	Human CDNA clone (
553	15	1.5	188	AAH65885	E. coli proliferat	c 626	15	387	22	AAH05361	Human reproductive	
554	15	1.5	188	AAH66134	E. coli proliferat	c 627	15	387	22	AAH05362	Human reproductive	
c 555	15	1.5	189	AAH00362	Human secreted pro	c 628	15	387	22	AAH05363	Human reproductive	
c 556	15	1.5	190	AAH51524	Human secreted pro	c 629	15	387	22	AAH56369	Human immune/haema	
c 557	15	1.5	223	AAH41501	Human secreted exp	c 630	15	387	23	ABL98230	Human testicular a	
c 558	15	1.5	242	AAH89201	Human brain T calc	c 631	15	387	23	ABL98231	Human testicular a	
559	15	1.5	256	AAH42664	Human secreted exp	c 632	15	387	23	ABL98232	Human testicular a	
560	15	1.5	259	AAH02730	Human secreted pro	c 633	15	388	20	AAH80216	Mouse nuclear rece	
561	15	1.5	259	AAH34224	Human prostate exp	c 634	15	389	23	AAH66063	DNA encoding novel	
562	15	1.5	259	AAH34224	Human prostate exp	635	15	394	24	ABN21877	Human ORFX polynuc	
563	15	1.5	261	AAH28672	Human secreted pro	636	15	396	22	AAH94947	Human ovarian can	
564	15	1.5	262	AAH38589	Novel human diagno	637	15	396	24	ABT03214	Human ovarian can	
c 565	15	1.5	263	AAH43023	Human secreted exp	638	15	396	24	ABL48897	Ovarian carcinoma	
c 566	15	1.5	265	AAH17394	Human prostate exp	639	15	397	22	AAH13874	Human breast cance	
567	15	1.5	269	AAH74535	Corn tassal-derive	640	15	397	22	AAH75097	Human immune/haema	
568	15	1.5	270	AAH19815	Human ORFX polynuc	c 641	15	400	18	AAV75813	Staphylococcus aur	
569	15	1.5	276	AAH67819	C Glutamicum codin	642	15	401	21	AAH77766	CDNA encoding huma	
570	15	1.5	282	AAH208794	Human src-family k	643	15	401	22	AAI28504	Colon tumour relat	
571	15	1.5	282	AAH14748	Src-family kinase	644	15	404	21	AAH22368	Human secreted pro	
572	15	1.5	283	AAH03934	Human prostate exp	645	15	407	21	AAH48571	CDNA encoding whea	
573	15	1.5	284	AAH74212	Loblolopy pine SSR	c 646	15	414	24	ABN60490	Human cancer relat	
c 574	15	1.5	287	AAH73774	Corn tassal-derive	c 647	15	417	23	AAI80650	Human polynucleoti	
c 575	15	1.5	291	AAH24675	Fragment of intron	648	15	418	24	ABL64342	Stomach cancer rel	
c 576	15	1.5	294	AAH08257	Human secreted pro	c 649	15	420	21	AAH93867	Cat flea hindgut a	
577	15	1.5	299	AAH09237	Fusarium venenatum	650	15	422	22	AAH22834	Human breast cance	
578	15	1.5	299	AAH32270	Human secreted pro	651	15	425	23	AAH86203	DNA encoding novel	
579	15	1.5	300	AAH13578	Human gene express	652	15	426	24	ABQ69740	Listeria innocua D	
c 581	15	1.5	301	AAH22612	Human ORFX polynuc	c 653	15	430	22	ABA56762	Human foetal liver	
c 582	15	1.5	303	AAH66038	E. coli proliferat	c 654	15	430	22	AAK30413	Human bone marrow	
c 583	15	1.5	303	AAH81331	Escherichia coli p	c 655	15	430	22	AAI15021	Probe #4954 for ge	
c 584	15	1.5	303	AAH84509	E. coli growth and	c 656	15	430	22	AAH415021	Human genome-deriv	
c 585	15	1.5	308	AAH52623	E. coli DNA for ce	657	15	436	24	ABD31387	Amplicon 22, 5'mox	
586	15	1.5	308	AAH00342	Human secreted pro	c 658	15	436	24	ABD31387	Amplicon 22, 5'mox	
587	15	1.5	309	AAH93954	Gene #452 used to	659	15	437	21	AAH47691	Arabidopsis thallia	
588	15	1.5	311	AAH40322	Human secreted pro	660	15	438	23	ABV46396	Human prostate exp	
589	15	1.5	314	AAH56273	Human immune/haema	661	15	441	21	AAH69742	Human breast tumou	
c 590	15	1.5	318	AAH92649	Staphylococcus epi	662	15	441	23	ABH18438	Human prostate exp	
c 591	15	1.5	321	AAH01540	Human reproductive	663	15	447	22	AAH67762	C glutamicum codin	
c 592	15	1.5	321	AAH96980	Human testicular a	c 664	15	450	22	AAH13972	Human breast cance	
c 593	15	1.5	330	AAH44776	Human polynucleoti	c 665	15	454	23	ABV04846	Human prostate exp	
c 594	15	1.5	332	ABV56463	Human prostate exp	c 666	15	455	21	AAH78096	CDNA encoding huma	
												Colon tumour relat

c 667	15	1.5	456	22	AAK31486	Human bone marrow	c 740	15	1.5	548	22	AAI39408	Probe #8094 used t
c 668	15	1.5	456	24	ABS06240	Human genome-deriv	c 741	15	1.5	548	24	ABS08578	Human genome-deriv
c 669	15	1.5	459	21	AAC00088	Human secreted pro	c 742	15	1.5	550	23	ABV31706	Human prostate exp
c 670	15	1.5	462	22	ABA006980	Human pancreatic c	c 743	15	1.5	550	23	ABV40674	Human prostate exp
c 671	15	1.5	462	22	AAK88181	Human digestive sy	c 744	15	1.5	550	24	ABQ27706	Oligonucleotide fo
c 672	15	1.5	462	23	ABL21521	Drosophila melanog	c 745	15	1.5	550	24	ABQ27707	Oligonucleotide fo
c 673	15	1.5	466	22	AAI10939	Human breast cance	c 746	15	1.5	550	24	ABQ27708	Oligonucleotide fo
c 674	15	1.5	467	24	ABK45360	cDNA encoding colo	c 747	15	1.5	550	24	ABQ27709	Oligonucleotide fo
c 675	15	1.5	470	22	ABA44423	Human breast cell	c 748	15	1.5	550	24	ABN61382	Human cancer relat
c 676	15	1.5	470	22	ABA54869	Human foetal liver	c 749	15	1.5	558	23	ABV52763	Human prostate exp
c 677	15	1.5	470	22	ABA24635	Probe #3101 for ge	c 750	15	1.5	558	23	ABV53702	Human prostate exp
c 678	15	1.5	470	22	AAK31146	Human brain expres	c 751	15	1.5	561	23	AA655785	DNA encoding novel
c 679	15	1.5	470	22	AAI13172	Probe #3105 for ge	c 752	15	1.5	570	22	AAH29494	Drosophila melanog
c 680	15	1.5	470	22	AAI03076	Probe #3067 used t	c 753	15	1.5	573	22	ABA59524	Human foetal liver
c 681	15	1.5	477	23	ABK42015	cDNA encoding nove	c 754	15	1.5	573	22	ABA28139	Probe #6605 for ge
c 682	15	1.5	477	23	ABV48223	Human prostate exp	c 755	15	1.5	573	22	AAK07797	Human brain expres
c 683	15	1.5	480	23	AA652295	DNA encoding novel	c 756	15	1.5	573	22	AAK33663	Human bone marrow
c 684	15	1.5	481	22	AAK32653	Human bone marrow	c 757	15	1.5	573	22	AAI16491	Probe #6424 for ge
c 685	15	1.5	481	22	AAI38468	Probe #7154 used t	c 758	15	1.5	573	23	ABV59158	Probe #8072 used t
c 686	15	1.5	481	24	ABS07444	Human genome-deriv	c 759	15	1.5	573	23	ABV59158	Human prostate exp
c 687	15	1.5	481	24	ABQ58368	Human colon cancer	c 760	15	1.5	573	24	ABS08562	Human genome-deriv
c 688	15	1.5	483	23	ABV13103	Human prostate exp	c 761	15	1.5	577	24	ABQ56010	Human ovarian anti
c 689	15	1.5	485	22	AAI18703	Human breast cance	c 762	15	1.5	580	22	ABA64253	Human foetal liver
c 690	15	1.5	486	20	AAK84692	Human metastatic m	c 763	15	1.5	580	22	ABA31394	Human brain expres
c 691	15	1.5	487	24	ABN65261	Human cancer relat	c 764	15	1.5	580	22	AAK12726	Human brain expres
c 692	15	1.5	489	22	AAI18384	Human breast cance	c 765	15	1.5	580	22	AAI19243	Probe #9176 for ge
c 693	15	1.5	489	22	AAK81368	Human immune/haema	c 766	15	1.5	580	22	ABS12608	Human genome-deriv
c 694	15	1.5	490	22	AAK81369	Human immune/haema	c 767	15	1.5	581	24	ABQ20898	Oligonucleotide fo
c 695	15	1.5	490	23	ABV50595	Human prostate exp	c 768	15	1.5	581	24	ABQ20899	Oligonucleotide fo
c 696	15	1.5	493	22	AA646999	Human breast cance	c 769	15	1.5	585	22	AAH67576	C glutamicum codin
c 697	15	1.5	493	22	ABF17569	Human breast cance	c 770	15	1.5	586	24	ABN64223	Human cancer relat
c 698	15	1.5	493	24	ABK95035	Human breast tumou	c 771	15	1.5	590	24	ABN64730	Human cancer relat
c 699	15	1.5	495	22	AAI99013	Human excretory re	c 772	15	1.5	591	20	AAK97629	Extended human sec
c 700	15	1.5	495	22	AAI63367	Human kidney relat	c 773	15	1.5	591	22	AAH05716	Human cDNA clone (
c 701	15	1.5	499	24	ABK77477	Bacillus clausii g	c 774	15	1.5	594	22	ABA59559	Human foetal liver
c 702	15	1.5	500	24	ABQ39468	Oligonucleotide fo	c 775	15	1.5	594	22	ABA28156	Probe #6622 for ge
c 703	15	1.5	500	24	ABQ39469	Oligonucleotide fo	c 776	15	1.5	594	22	AAK07833	Human brain expres
c 704	15	1.5	501	23	AA686127	DNA encoding novel	c 777	15	1.5	594	22	AAK33699	Human bone marrow
c 705	15	1.5	501	21	AAK53591	Arabidopsis thalia	c 778	15	1.5	594	22	AAI39422	Probe #8108 used t
c 706	15	1.5	505	21	AAK08711	Fusarium venenatum	c 779	15	1.5	594	24	ABS08587	Human genome-deriv.
c 707	15	1.5	511	21	AAK52449	Arabidopsis thalia	c 780	15	1.5	605	23	ABV50611	Human prostate exp
c 708	15	1.5	511	22	AAI19732	Human breast cance	c 781	15	1.5	605	24	ABQ58733	Human colon cancer
c 709	15	1.5	514	22	ABA61776	Human foetal liver	c 782	15	1.5	610	21	AAK11466	Aspergillus niger
c 710	15	1.5	514	22	ABA29382	Probe #7848 for ge	c 783	15	1.5	612	23	ABV56242	Human prostate exp
c 711	15	1.5	514	22	AAK10088	Human brain expres	c 784	15	1.5	614	23	ABL14137	Drosophila melanog
c 712	15	1.5	514	22	AAK35982	Human bone marrow	c 785	15	1.5	617	24	ABQ27636	Oligonucleotide fo
c 713	15	1.5	514	22	AAI17195	Probe #10382 used	c 786	15	1.5	617	24	ABQ27637	Oligonucleotide fo
c 714	15	1.5	514	22	AAI41696	Human genome-deriv	c 787	15	1.5	618	24	ABQ37458	Oligonucleotide fo
c 715	15	1.5	514	24	ABS10171	Human immune/haema	c 788	15	1.5	618	24	ABQ37459	Oligonucleotide fo
c 716	15	1.5	518	22	AAK61942	Human immune/haema	c 789	15	1.5	621	23	ABL29063	Drosophila melanog
c 717	15	1.5	520	24	ABQ25322	Oligonucleotide fo	c 790	15	1.5	621	23	ABN61324	Human cancer relat
c 718	15	1.5	520	24	ABQ25323	Oligonucleotide fo	c 791	15	1.5	627	24	ABN61324	C glutamicum codin
c 719	15	1.5	521	22	AAH81622	Human differential	c 792	15	1.5	636	22	AAH67699	Human prostate exp
c 720	15	1.5	521	24	ABQ24696	Oligonucleotide fo	c 793	15	1.5	637	23	ABV18187	Oligonucleotide fo
c 721	15	1.5	521	24	ABQ24697	Oligonucleotide fo	c 794	15	1.5	637	24	ABQ44658	Oligonucleotide fo
c 722	15	1.5	521	24	ABQ30308	Oligonucleotide fo	c 795	15	1.5	637	24	ABQ44659	Oligonucleotide fo
c 723	15	1.5	521	24	ABQ30309	Oligonucleotide fo	c 796	15	1.5	639	23	ABV58459	Human prostate exp
c 724	15	1.5	521	24	ABQ30309	Oligonucleotide fo	c 797	15	1.5	641	23	ABV47975	Human prostate exp
c 725	15	1.5	522	24	ABQ59375	Human colon cancer	c 798	15	1.5	645	20	AAK97768	Extended human sec
c 726	15	1.5	528	24	ABQ29880	Oligonucleotide fo	c 799	15	1.5	647	21	AAK59758	Human secreted pro
c 727	15	1.5	528	24	ABQ29881	Oligonucleotide fo	c 800	15	1.5	648	21	AAK97768	Helicobacter pylor
c 728	15	1.5	530	20	AAK20913	Polynucleotide seq	c 801	15	1.5	652	24	ABQ58497	Human colon cancer
c 729	15	1.5	533	23	ABV50889	Human prostate exp	c 802	15	1.5	652	24	ABK09619	Human ovarian tumo
c 730	15	1.5	534	24	ABN73537	Bovine embryonic g	c 803	15	1.5	652	24	ABK09619	Human colon cancer
c 731	15	1.5	535	21	AAK280214	Human colon cancer	c 804	15	1.5	654	24	ABQ58444	Human colon cancer
c 732	15	1.5	536	23	ABV01367	Human prostate exp	c 805	15	1.5	657	24	ABQ59017	Nucleotide sequenc
c 733	15	1.5	538	24	ABQ38002	Oligonucleotide fo	c 806	15	1.5	658	20	AAK15920	DNA encoding novel
c 734	15	1.5	538	24	ABQ38003	Oligonucleotide fo	c 807	15	1.5	663	24	ABK33315	Oligonucleotide fo
c 735	15	1.5	542	24	ABK45851	cDNA encoding colo	c 808	15	1.5	665	24	ABQ26684	Oligonucleotide fo
c 736	15	1.5	544	24	ABQ36756	Oligonucleotide fo	c 809	15	1.5	665	24	ABQ26684	Oligonucleotide fo
c 737	15	1.5	544	24	ABQ36757	Oligonucleotide fo	c 810	15	1.5	669	21	AAK51175	Murine olfactory r
c 738	15	1.5	548	22	ABA59546	Human foetal liver	c 811	15	1.5	673	20	AAK13641	Enterococcus faeca
c 739	15	1.5	548	22	AAK07819	Human brain expres	c 812	15	1.5	679	21	AAK12290	Aspergillus oryzae
c 740	15	1.5	548	22	AAK33685	Human bone marrow	c 813	15	1.5	679	22	AAH99104	Yeast EST-derived
c 741	15	1.5	548	22	AAK33685	Human bone marrow	c 814	15	1.5	684	22	AAH08029	Human cDNA clone (

c 959 15 1.5 1242 21 AAAG2991 Human beta2-adrenergic
 960 15 1.5 1242 23 AAS71485 DNA encoding novel
 961 15 1.5 1248 23 ABL25803 Drosophila melanog
 962 15 1.5 1248 24 AAD21998 Human transporters
 963 15 1.5 1255 23 AAS86210 DNA encoding novel
 964 15 1.5 1258 24 AAS94877 Human DNA sequence
 965 15 1.5 1262 21 AAD36247 Human TWIK-9 cDNA
 966 15 1.5 1266 24 AAC51603 Arabidopsis thalia
 967 15 1.5 1266 22 AAH52375 S. epidermidis ope
 968 15 1.5 1267 21 AAC77794 Human cancer assoc
 969 15 1.5 1287 12 AAQ13381 Human beta2-adrenergic
 970 15 1.5 1300 20 AAZ09352 Plasmid pUSlim DNA
 971 15 1.5 1302 24 ABK75350 Bacillus lichenifo
 972 15 1.5 1305 21 AAC54212 Arabidopsis thalia
 973 15 1.5 1305 23 AAS89621 DNA encoding novel
 974 15 1.5 1310 19 AAV52399 Streptococcus pneu
 975 15 1.5 1311 24 ABN90923 Staphylococcus epi
 976 15 1.5 1319 21 AAB38558 Actinobacillus ple
 977 15 1.5 1320 21 AAC43225 Arabidopsis thalia
 978 15 1.5 1330 21 AAC41175 Arabidopsis thalia
 979 15 1.5 1330 22 AAH23816 Human transferase
 980 15 1.5 1335 24 ABN66154 Streptococcus poly
 981 15 1.5 1340 21 AAC69477 Human secreted pro
 982 15 1.5 1346 24 ABN81333 Physcomitrella pat
 983 15 1.5 1347 22 AAF60981 P. putida KT240-a
 984 15 1.5 1353 11 AAQ05667 PMS10 contg. male
 985 15 1.5 1353 11 AAQ05759 cDNA clone pMS10 e
 986 15 1.5 1353 11 AAQ08572 cDNA clone pMS10 e
 987 15 1.5 1353 11 AAQ08544 cDNA clone pMS10 e
 988 15 1.5 1353 18 AAT60952 Anther-specific cD
 989 15 1.5 1355 21 AAC46835 Arabidopsis thalia
 990 15 1.5 1356 23 ABL27439 Drosophila melanog
 991 15 1.5 1358 24 AAS62425 Human secreted pro
 992 15 1.5 1370 21 AAA26413 DNA encoding human
 993 15 1.5 1374 22 AAS40754 Human reproductive
 994 15 1.5 1374 22 AAL07400 Human reproductive
 995 15 1.5 1375 22 AAS40755 DNA encoding human
 996 15 1.5 1375 22 AAS40756 DNA encoding human
 997 15 1.5 1375 22 AAL07401 Human reproductive
 998 15 1.5 1375 22 AAL07402 Human reproductive
 999 15 1.5 1379 23 AAS72805 DNA encoding novel
 1000 15 1.5 1382 23 ABV25632 Human prostate exp

ALIGNMENTS

RESULT 1
 AAN80494
 ID AAN80494 standard; DNA; 1234 BP.

XX AC AAN80494;

XX DT 29-NOV-1990 (first entry)

XX DE Sequence encoding human testis-specific lactate dehydrogenase subunit.

XX KW Testis-specific lactate dehydrogenase; vaccine; female fertility; ss.

XX OS synthetic.

XX FH Key Location/Qualifiers
 XX FT CDS 76..1083
 XX FT /*tag= a
 XX FT /label=LDH-C4

XX PN EP270056-A.

XX PD 08-JUN-1988.

XX PF 30-NOV-1987; 87EP-0117688.

XX PR 12-JUN-1987; 87US-0061894.

PR 12-JUN-1987; 87US-0936451.
 XX PA (NOUN) NORTHWESTERN UNIV.
 XX PI Goldberg E, Millan JL;
 XX DR WPI; 1988-156290/23.
 XX DR P-PSDB; AAF80891.
 XX New recombinant DNA encoding sub-unit of testis lactate dehydrogenase -
 PT expressing antigenic polypeptide useful in vaccines for reducing
 PT female fertility.
 XX PS Disclosure; ; pp; English.
 XX CC This encodes a testis-specific lactate dehydrogenase sub-unit (LDH-C4).
 CC The complete subunit or one or more antigenic regions can be used in a
 CC vaccine prepn. to reduce female fertility. Larger peptides (or fusion
 CC proteins) expressed by this DNA are antigenic and smaller peptides be-
 CC come so when coupled to e.g. tetanus toxoid.
 XX SQ Sequence 1234 BP; 366 A; 202 C; 286 G; 380 T; 0 other;
 Query Match 2.1%; Score 20; DB 9; Length 1234;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 547 ATTGGAGAACATGGTGATTC 566
 Db 643 ATTGGAGAACATGGTGATTC 662
 RESULT 2
 AAS17494
 ID AAS17494 standard; cDNA; 1680 BP.
 XX AC AAS17494;
 XX DT 26-FEB-2002 (first entry)
 XX DE Human cDNA encoding testicular lactate dehydrogenase A.
 XX KW Human; ss; testicular lactate dehydrogenase A; fusion protein;
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 99..1244
 XX FT /*tag= a
 XX FT /product= "Testicular lactate dehydrogenase A"
 XX PN CN1313342-A.
 XX PD 19-SEP-2001.
 XX PF 28-FEB-2001; 2001CN-0108262.
 XX PR 28-FEB-2001; 2001CN-0108262.
 XX (UYNA-) UNIV NANJING MEDICAL.
 XX Sha J, Zhou Z, Li J;
 XX WPI; 2002-042206/06.
 XX DR P-PSDB; AAU11432.
 XX PT New human testis lactate dehydrogenase A for preparing monoclonal and
 PT multiclonal antibodies -
 XX Claim 4; Page 1-2; 6pp; Chinese.
 XX CC The invention relates to a human testicular novel lactate dehydrogenase

CC present sequence is a GENSET nucleic acid of the invention.

XX Sequence 1755 BP; 514 A; 343 C; 379 G; 519 T; 0 other;

SQ Query Match 2.0%; Score 19; DB 22; Length 1755;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 19; Conservative 0; Mismatches 0; Indels

Qy 471 TCTGGATACTGCTCGTTTT 489

Db 737 TCTGGATACTGCTCGTTTT 755

RESULT 4

AAH64738

ID AAH64738 standard; cDNA; 1759 BP.

XX AC AAH64738;

XX 11-SEP-2001 (first entry)

DT Human secreted protein cDNA, SEQ ID NO: 14.

DE Human; secreted protein; gene therapy; vaccine; treatment; d;

KW GENSET; ss.

XW Homo sapiens.

OS WO200142451-A2.

PN 14-JUN-2001.

PD 07-DEC-2000; 2000WO-1B01938.

PF 08-DEC-1999; 99US-0169629.

PR 06-MAR-2000; 2000US-0187470.

XX (GEST) GENSET.

PA Dumas Milne Edwards J, Bougueleret L, Jobert S;

PI WPI; 2001-367870/38.

XX P-PSDB; AAG89135.

DR Full length GENSET human nucleic acids encoding potentially

PT proteins, useful in gene therapy and vaccination against a v

PT diseases, and for diagnosis of those diseases -

XX Claim 7; Page 572-574; 921pp; English.

XX The invention relates to full length GENSET human nucleic ac

CC potentially secreted proteins. The nucleic acids and the pol

CC they encode may be used in the prevention, treatment and dia

CC diseases associated with inappropriate GENSET gene expression

CC example, they be used to treat disorders associated with dec

CC GENSET gene expression by rectifying mutations or deletions

CC patient's genome that affect the activity of GENSET or by su

CC the patients own production of GENSET polypeptides. Converse

CC antisense nucleic acid molecules may be administered to down

CC GENSET expression by binding with the cells' own genes and p

CC their expression. The sense and antisense nucleic acids may

CC used as DNA probes in diagnostic assays to detect and quanti

CC presence of similar nucleic acid sequences in samples, and h

CC determine which patients may be in need of restorative ther

CC The GENSET polypeptides may be used as antigens in the produ

CC antibodies and in assays to identify modulators (agonists an

CC antagonists) of GENSET polypeptide expression and activity.

XX present sequence is a GENSET nucleic acid of the invention.

SQ Sequence 1759 BP; 515 A; 344 C; 379 G; 521 T; 0 other;

XX Query Match 2.0%; Score 19; DB 22; Length 1759;

Best Local Similarity 100.0%; Pred. No. 18;

```
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 471 TCTGACTACTGCTGCTTTT 489
Db 739 TCTGACTACTGCTGCTTTT 757

RESULT 5
AADI4466
ID AADI4466 standard; cDNA; 4068 BP.
XX AC AADI4466;
XX DT 01-NOV-2001 (first entry)
XX DE Mouse p97 (mp97) protein cDNA.
XX KW Mouse; mp97 protein; scialoglycoprotein; neuroprotective; antibacterial;
XX KW analgesic; nootropic; cytostatic; neuroleptic; virucide; anticonvulsant;
XX KW deficiency disease; Wernicke's disease; neurodegenerative disease; pain;
XX KW nutritional polyneuropathy; neurological disorder; cancer; gene therapy;
XX KW Huntington's disease; Alzheimer's disease; Parkinson's disease; epilepsy;
XX KW demyelinating disease; multiple sclerosis; amyotrophic lateral sclerosis;
XX KW psychosis; therapeutic; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 64..2280
XX FT /tag= a
XX FT /product= "Mouse p97 protein"
XX FT sig_peptide 64..120
XX FT /tag= b
XX FT mat_peptide 121..2277
XX FT /tag= c
XX FT /product= "Mature mouse p97 protein"
XX FT 5'UTR 1..63
XX FT /tag= d
XX FT /note= "5' untranslated region (UTR)"
XX FT 3'UTR 2281..4068
XX FT /tag= e
XX FT /note= "3' untranslated region (UTR)"
XX FT polyA_signal 3299..3304
XX FT /tag= f
XX FT /note= "Polyadenylation signal I"
XX FT polyA_site 3544
XX FT /tag= g
XX FT /note= "Polyadenylation site I"
XX FT polyA_signal 3106..3111
XX FT /tag= h
XX FT /note= "Polyadenylation signal II"
XX FT polyA_site 3128
XX FT /tag= i
XX FT /note= "Polyadenylation site II"
XX FT polyA_signal 4028..4033
XX FT /tag= j
XX FT /note= "Polyadenylation signal for EST2 transcript"
XX FT polyA_site 4048
XX FT /tag= k
XX FT /note= "Polyadenylation site for EST2 transcript"
XX FT polyA_signal 4049..4068
XX FT /tag= l
XX FT /note= "Polyadenylation tail"
XX FT
XX PN WO200159459-A2.
XX PD 16-AUG-2001.
XX PF 08-FEB-2001; 2001WO-CA00133.
XX PR 08-FEB-2000; 2000US-0181091.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.

Cheng N, Gagnier L, Jefferies WA;
WPI; 2001-514683/56.
P-PSDB; AAE06668.
Novel murine p97 polypeptides and polynucleotides for preparing
experimental models to study murine p97 and to identify modulators of
murine p97 expression or activity useful for treating neurological
conditions -
Claim 25; Page 53-54; 70pp; English.
The invention relates to mouse p97 protein, mp97 (a scialoglycoprotein)
and its corresponding cDNA molecule. Mouse p97 protein and its cDNA
molecule are useful for identifying compounds that affects mp97 protein
activity or expression. The invention also relates to a method for
screening therapeutic agents which are useful for treating neurological
conditions, such as cancer, neurodegenerative diseases (e.g., Alzheimer's
disease, Parkinson's disease, Huntington's disease), demyelinating
diseases (e.g., multiple sclerosis), amyotrophic lateral sclerosis,
bacterial and viral infections, deficiency diseases (e.g., Wernicke's
disease, nutritional polyneuropathy), epilepsy, psychosis, pain and
neurological disorders, especially Alzheimer's disease. Mouse p97 DNA's
are also useful in gene therapy. Mp97 proteins are useful for delivering
therapeutic agents and pharmaceuticals across the blood placenta barrier
as well as to other organs including liver. The invention is also useful
for preparing antibodies and antisense oligonucleotides, the preparation
of experimental systems to study mp97, and in diagnostic and therapeutic
applications. Transgenic p97 mice is useful for identifying essential
physiological roles for p97 in development and adult functioning of the
organism and for testing potential therapeutic and diagnostic agents that
are conjugated to p97 protein. The present cDNA sequence encodes mouse
p97 (mp97) protein.
Query Match 2.0%; Score 19; DB 22; Length 4068;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 803 CCCTGCTGATTATTTGG 821
Db 551 CCCTGCTGATTATTTGG 569
RESULT 6
AAF62198
ID AAF62198 standard; DNA; 4158 BP.
XX AC AAF62198;
XX DT 21-MAY-2001 (first entry)
XX DE DNA encoding membrane bound transferrin like protein.
XX KW Chondrogenesis promoter; membrane-bound transferrin-like protein; Mtf;
XX KW Chondrogenesis regulator; Mtf activator; bone metabolism; mouse;
XX KW Chondral differentiation inhibitor; bone disease; ds.
XX OS Mus sp.
XX PN WO200113951-A1.
XX PD 01-MAR-2001.
XX PF 21-AUG-2000; 2000WO-JP05590.
XX PR 19-AUG-1999; 99JP-0232966.
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX PI Kato Y, Fujimoto K;
```

XX WPI; 2001-218409/22.
DR P-PSDB; AAB62882.
XX
PT Chondrogenesis promoters containing membrane-bound transferrin-like
PT protein, useful in diagnosis, prevention and treatment of diseases due
PT to abnormal chondral metabolism and bone metabolism -
XX
XX Disclosure; Page 43-46; 57pp; Japanese.
PS
PS This invention relates to chondrogenesis promoters containing a
CC membrane-bound transferrin-like protein (MTF). Chondrogenesis promoters,
CC chondrogenesis regulators, MTF activators, MTF antagonist-containing
CC chondral differentiation inhibitors are useful in diagnosis, prevention
CC and treatment of diseases due to abnormal chondral metabolism and bone
CC metabolism e.g. bone diseases. The present sequence represents murine DNA
CC encoding MTF.
XX
XX Sequence 4158 BP; 960 A; 1159 C; 1177 G; 862 T; 0 other;
SQ
Query Match 2.0%; Score 19; DB 22; Length 4158;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 803 CCGTGGTGATTTATTTGG 821
DB 605 CCGTGGTGATTTATTTGG 623
RESULT 7
ABL28478
ID ABL28478 standard; DNA; 5313 BP.
XX
AC ABL28478;
XX
DT 26-MAR-2002 (first entry)
DE
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36907.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
PN
PN 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX Claim 1; SEQ ID NO 36907; 21pp + Sequence Listing; English.
PS
PS The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5313 BP; 1472 A; 1219 C; 1230 G; 1392 T; 0 other;
Query Match 2.0%; Score 19; DB 23; Length 5313;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58 GTGGTAGTGGAGTGGAA 76
DB 5108 GTGGTAGTGGAGTGGAA 5126
RESULT 8
AAF28536
ID AAF28536 standard; DNA; 33140 BP.
XX
AC AAF28536;
XX
DT 04-APR-2001 (first entry)
XX
DE Genomic fragment #23.
XX
XX Genomic library; bacteria; human upper airway; otitis media; sinusitis;
KW bronchopulmonary; endocarditis; meningitis; ss.
XX
OS Moraxella catarrhalis.
XX
XX WO200078968-A2.
PN
XX 28-DEC-2000.
PD
PF 16-JUN-2000; 2000WO-US16649.
XX
PR 18-JUN-1999; 99US-0140121.
XX
PA (INCY-) INCYTE GENOMICS INC.
PI
PI Lagace RE, Patterson C, Berg KL;
XX
XX WPI; 2001-041427/05.
DR
XX Genomic library for identifying diagnostic and therapeutic
PT compositions, and for identifying virulence factors, regulatory
PT elements and drug targets, comprises Moraxella catarrhalis nucleic
PT acids -
XX
PS Claim 1; Page 191-199; 545pp; English.
XX
XX The present invention relates to a Moraxella catarrhalis genomic library
CC comprising of a combination of 41 nucleic acid molecules (see
CC AAF28514-AAF28554). The library has a number of uses described in the
CC specification e.g. is useful for identifying diagnostic and therapeutic
CC compositions. M. catarrhalis (Branhamella catarrhalis) is a large
CC aerobic, gram-negative diplococcus, normally found among the bacterial
CC flora of human upper airways. M. catarrhalis is known to cause acute,
CC localised infections such as otitis media, sinusitis and bronchopulmonary
CC infection and life-threatening, systemic diseases including endocarditis
CC and meningitis.
XX
SQ Sequence 33140 BP; 9472 A; 6496 C; 7384 G; 9787 T; 1 other;
Query Match 2.0%; Score 19; DB 22; Length 33140;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 908 AAATAGATTGATGGA 926
DB 9745 AAATAGATTGATGGA 9763

RESULT 9

AAF22305
ID AAF22305 standard; DNA; 1082138 BP.
XX
XX AAF22305;
AC
XX
XX 20-MAR-2001 (first entry)
DT
XX
XX Arabidopsis thaliana chromosome 4 centromere.
DE
XX
XX Centromere; microsome; vector; ds.
KW
XX
XX Arabidopsis thaliana.
OS
XX
XX WO200055325-A2.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 17-MAR-2000; 2000WO-US07392.
PF
XX
XX 18-MAR-1999; 99US-0125219.
PR
XX
XX 01-APR-1999; 99US-0127409.
PR
XX
XX 18-MAY-1999; 99US-0134770.
PR
XX
XX 13-SEP-1999; 99US-0153584.
PR
XX
XX 17-SEP-1999; 99US-0154603.
PR
XX
XX (UYCH-) UNIV CHICAGO.
PA

XX Preuss D, Copenhaver G, Keith K;
XX
XX WPI; 2000-587529/55.
XX
XX

XX Recombinant DNA construct comprising a plant centromere, useful for
XX producing stably inherited microsome which can serve as vectors for
XX the construction of transgenic plant and animal cells
XX
XX

XX Claim 68; Page 977-1388; 1449pp; English.
XX
XX

XX The present invention relates to a recombinant DNA construct of a plant
XX (Arabidopsis thaliana) centromere. The constructs are useful for
XX producing stably inherited microsome which can serve as vectors for
XX the construction of transgenic plant and animal cells expressing
XX selected proteins such as hormones, enzymes, interleukins, clotting
XX factors, cytokines, antibodies, and growth factors.
XX
XX

XX Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
SQ

Query Match 2.0%; Score 19; DB 21; Length 1082138;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 908 AATAGATTGATGAAAA 926
|||||

Db 451974 AATAGATTGATGAAAA 451992
|||||

RESULT 10

ABL19001/C
ID ABL19001 standard; DNA; 360 BP.
AC
XX
XX ABL19001;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 8476.
XX

XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX

XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX

PD 27-SEP-2001.
XX

PF 23-MAR-2001; 2001WO-US09231.
XX

XX 23-MAR-2000; 2000US-191637P.
PR

PR 11-JUL-2000; 2000US-0614150.
XX

XX (PEKE) PE CORP NY.
PA

XX Venter JC, Adams M, Li PWD, Myers BW;
PI

XX WPI; 2001-656860/75.
DR

XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions
PT

XX Claim 1; SEQ ID NO 8476; 21pp + Sequence Listing; English.
PS

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABBS7737-ABBS72072).
CC

XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
CC

XX Sequence 360 BP; 105 A; 76 C; 101 G; 78 T; 0 other;
SQ

Query Match 1.9%; Score 18; DB 23; Length 360;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 468 AGTTCGGATCTGCTCG 485
|||||

Db 107 AGTTCGGATCTGCTCG 90
|||||

RESULT 11

AAF07721/C
ID AAF07721 standard; cDNA; 644 BP.
XX

XX AAF07721;
AC

XX 13-MAR-2001 (first entry)
DT

XX Fusarium venenatum EST SEQ ID NO:244.
DE

XX Multiple gene expression; filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.
XX

OS Fusarium venenatum.
XX

XX WO200056762-A2.
XX

XX 28-SEP-2000.
PD

XX 22-MAR-2000; 2000WO-US07781.
XX

XX 22-MAR-1999; 99US-0273623.
PR

XX (NOVO) NOVO NORDISK BIOTECH INC.
PA

XX (NOVO) NOVO NORDISK AS.
PA

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
PI
XX

DR WPI; 2000-594572/56.
 XX Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX Claim 86; Page 476; 3161pp; English.
 XX The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAP07478 to AAP11247 represents ESTs from
 CC Fusarium venenatum; AAP11248 to AAP11853 represents ESTs from Aspergillus
 CC niger; AAP11854 to AAP14878 represents ESTs from Aspergillus oryzae; and
 CC AAP14879 to AAP15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX
 SQ Sequence 644 BP; 174 A; 190 C; 140 G; 132 T; 8 other;
 Query Match 1.9%; Score 18; DB 21; Length 644;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 805 GTTGGTGATTATTTGGG 822
 DB 23 GTTGGTGATTATTTGGG 6
 RESULT 12
 ABK79311/c
 ID ABK79311 standard; DNA; 828 BP.
 XX
 AC ABK79311;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Bacillus clausii genomic sequence tag (GST) #2154.
 XX
 KW Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 XX
 OS Bacillus clausii.
 XX
 PN WO200229113-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31437.
 XX
 PR 06-OCT-2000; 2000US-0680598.
 PR 27-MAR-2001; 2001US-279526P.
 XX
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 XX
 XX Berka R, Clausen IG;
 PI

XX WPI; 2002-416684/44.
 DR Monitoring differential expression of several genes in first Bacillus
 XX cell relative to expression of same genes in one or more second
 PT Bacillus cells, by using substrate containing Bacillus genomic
 PT sequenced tag array -
 XX Claim 11; SEQ ID NO 6602; 200pp; English.
 XX The invention describes a method of monitoring differential expression of
 CC genes in a first Bacillus cell relative to expression of the genes in
 CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
 CC isolated from Bacillus cells to a substrate containing array of Bacillus
 CC genomic sequenced tags (GST), examining the array, and determining
 CC relative gene expression by an observed hybridisation reporter signal of
 CC a spot in the array. The method is useful for measuring the expression of
 CC genes in a first Bacillus cell relative to expression of the same genes
 CC in one or more second Bacillus cells. The method is useful for monitoring
 CC global expression of several genes from a Bacillus cell, discovering new
 CC genes, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which Bacillus cells adapt to changes in culture conditions,
 CC environmental stress or other physiological provocation. Extensive
 CC follow-up characterisation is unnecessary, when one spot on an array
 CC equals one gene or one open reading frame, since sequence information is
 CC available. This sequence represents a genomic sequence tag (GST) used in
 CC the method of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 828 BP; 277 A; 136 C; 186 G; 229 T; 0 other;
 Query Match 1.9%; Score 18; DB 24; Length 828;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 346 AATGTGCCAAATATGCT 363
 DB 291 AATGTGCCAAATATGCT 274
 RESULT 13
 AAS90935/c
 ID AAS90935 standard; cDNA; 1393 BP.
 XX
 AC AAS90935;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #26739.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; as.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 PI

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DR WPI; 2001-639362/73.
DR P-PSDB; ABG26749.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID No 26739; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1393 BP; 352 A; 352 C; 356 G; 333 T; 0 other;

Query Match 1.9%; Score 18; DB 23; Length 1393;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAAGATACAAAGTCTC 22
Db 146 TCCAAGATACAAAGTCTC 129

RESULT 14
AAZ37126
ID AAZ37126 standard; DNA; 1728 BP.
XX
XX AAZ37126;
XX
XX 28-JAN-2000 (first entry)
XX
XX Nucleotide sequence of H.influenzae HI1655 gene.
XX
XX Genome; mutagenesis; transposon; isolate; locate; essential gene; ss;
XX detect; growth; anti-microbial therapy; genomic footprinting.
XX
XX Haemophilus influenzae.
XX
XX WO9950402-A1.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US061139.
XX
XX 27-MAR-1998; 98US-0079770.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Mekalanos JJ, Akerley B, Rubin E, Camilli A;
XX WPI; 1999-620065/53.
XX
XX Detection of genes essential for the growth and viability of organism,

useful as e.g. targets for anti-microbial therapy
XX
XX Disclosure; Fig 5N; 62pp; English.
XX
XX Nucleotide sequences AAZ37113-237126 are essential Haemophilus
CC influenzae genes that have been identified by the methods of the
CC invention. The invention relates to a method for locating essential
CC regions of a portion of an organism's genome by: (i) in vitro
CC mutagenising DNA having the sequence of the region with a transposon;
CC (ii) identifying cells of the organism transformed with the mutagenised
CC DNA of (i); and (iii) locating the region by detecting the absence of
CC transposons in the region of the mutagenised cells containing the
CC mutagenised DNA. The invention also relates to a method for isolating a
CC compound that modulates the expression of a nucleic acid sequence
CC operably linked to a gene promoter, and a method of identifying a nucleic
CC acid sequence that is essential for cell growth or viability. The methods
CC are used to detect genes that are essential for the growth and viability
CC of organism. Such genes can be used e.g. as targets for anti-microbial
CC therapy.
XX
XX Sequence 1728 BP; 574 A; 332 C; 343 G; 479 T; 0 other;

Query Match 1.9%; Score 18; DB 20; Length 1728;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 TGCTGCAAAAATGCCAA 323
Db 324 TGCTGCAAAAATGCCAA 341

RESULT 15
AAZ41742/c
ID AAZ41742 standard; DNA; 1947 BP.
XX
XX AAZ41742;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 32967.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX
XX 05-MAR-1999; 99US-0123180.
XX
XX 09-MAR-1999; 99US-0123548.
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XX 23-MAR-1999; 99US-0125788.
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XX 25-MAR-1999; 99US-0126264.
XX
XX 01-APR-1999; 99US-0126785.
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XX 06-APR-1999; 99US-0127462.
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XX 08-APR-1999; 99US-0128234.
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XX 16-APR-1999; 99US-0128714.
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XX 19-APR-1999; 99US-0129845.
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XX 21-APR-1999; 99US-0130077.
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XX 23-APR-1999; 99US-0130449.
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XX 28-APR-1999; 99US-0130891.
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XX 30-APR-1999; 99US-0131449.
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XX 30-APR-1999; 99US-0132048.
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XX 04-MAY-1999; 99US-0132407.
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XX 05-MAY-1999; 99US-0132484.
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XX 06-MAY-1999; 99US-0132485.
XX
XX 99US-0132486.

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PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139492.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 28-SEP-1999; 99US-0156596.
PR 03-OCT-1999; 99US-0157117.
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 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 1.9%; Score 18; DB 21; Length 1947;
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 885 TGAACCTTCACCTCGATGA 902
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 Db 1147 TGAACCTTCACCTCGATGA 1130

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-992-430B-21

Perfect score: 972

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	18	1.9	29604	3	US-08-781-891-207
4	17	1.7	193	1	US-08-248-474-44
5	17	1.7	193	3	US-08-756-849-44
6	17	1.7	402	4	US-09-315-794-61
7	17	1.7	402	4	US-09-389-341-61
8	17	1.7	965	4	US-09-173-300-16
9	17	1.7	993	4	US-09-134-001C-1491
10	17	1.7	1112	1	US-08-136-743B-1
11	17	1.7	1240	3	US-08-869-506-1
12	17	1.7	1240	3	US-09-128-967-1
13	17	1.7	1315	4	US-09-234-186-2
14	17	1.7	1315	4	US-09-234-186-4
15	17	1.7	1315	4	US-09-234-186-5
16	17	1.7	1315	4	US-09-234-186-6
17	17	1.7	1315	4	US-09-233-527-2
18	17	1.7	1315	4	US-09-233-527-3
19	17	1.7	1315	4	US-09-233-527-5
20	17	1.7	1315	4	US-09-233-527-6
21	17	1.7	1315	5	PCT-US93-05651-2
22	17	1.7	1404	3	US-08-961-083-9
23	17	1.7	1524	1	US-08-409-122-1
24	17	1.7	1524	2	US-08-408-669-1
25	17	1.7	1954	4	US-09-370-807-3
26	17	1.7	1954	4	US-09-921-259-3
27	17	1.7	2387	1	US-08-288-408-4
28	C	100			Sequence 4, Appli
29	C	100			Sequence 125, App
30	C	100			Sequence 3, Appli
31	C	100			Sequence 8, Appli
32	C	100			Sequence 1, Appli
33	C	100			Sequence 1, Appli
34	C	100			Sequence 1, Appli
35	C	100			Sequence 166, App
36	C	100			Sequence 166, App
37	C	100			Sequence 166, App
38	C	100			Sequence 166, App
39	C	100			Sequence 166, App
40	C	100			Sequence 166, App
41	C	100			Sequence 166, App
42	C	100			Sequence 166, App
43	C	100			Sequence 166, App
44	C	100			Sequence 166, App
45	C	100			Sequence 166, App
46	C	100			Sequence 166, App
47	C	100			Sequence 166, App
48	C	100			Sequence 166, App
49	C	100			Sequence 166, App
50	C	100			Sequence 166, App
51	C	100			Sequence 166, App
52	C	100			Sequence 166, App
53	C	100			Sequence 166, App
54	C	100			Sequence 166, App
55	C	100			Sequence 166, App
56	C	100			Sequence 166, App
57	C	100			Sequence 166, App
58	C	100			Sequence 166, App
59	C	100			Sequence 166, App
60	C	100			Sequence 166, App
61	C	100			Sequence 166, App
62	C	100			Sequence 166, App
63	C	100			Sequence 166, App
64	C	100			Sequence 166, App
65	C	100			Sequence 166, App
66	C	100			Sequence 166, App
67	C	100			Sequence 166, App
68	C	100			Sequence 166, App
69	C	100			Sequence 166, App
70	C	100			Sequence 166, App
71	C	100			Sequence 166, App
72	C	100			Sequence 166, App
73	C	100			Sequence 166, App
74	C	100			Sequence 166, App
75	C	100			Sequence 166, App
76	C	100			Sequence 166, App
77	C	100			Sequence 166, App
78	C	100			Sequence 166, App
79	C	100			Sequence 166, App
80	C	100			Sequence 166, App
81	C	100			Sequence 166, App
82	C	100			Sequence 166, App
83	C	100			Sequence 166, App
84	C	100			Sequence 166, App
85	C	100			Sequence 166, App
86	C	100			Sequence 166, App
87	C	100			Sequence 166, App
88	C	100			Sequence 166, App
89	C	100			Sequence 166, App
90	C	100			Sequence 166, App
91	C	100			Sequence 166, App
92	C	100			Sequence 166, App
93	C	100			Sequence 166, App
94	C	100			Sequence 166, App
95	C	100			Sequence 166, App
96	C	100			Sequence 166, App
97	C	100			Sequence 166, App
98	C	100			Sequence 166, App
99	C	100			Sequence 166, App
100	C	100			Sequence 166, App

101	15	1.5	1411	4	US-09-387-574-1	Sequence 1, Appli	C 174	14	1.4	48	3	US-08-369-822C-37	Sequence 37, Appl
102	15	1.5	1411	4	US-09-668-096-1	Sequence 1, Appli	C 175	14	1.4	48	3	US-08-582-776C-52	Sequence 52, Appl
103	15	1.5	1491	2	US-09-006-675-1	Sequence 1, Appli	C 176	14	1.4	48	3	US-08-434-831B-49	Sequence 49, Appl
104	15	1.5	1491	2	US-09-228-603A-1	Sequence 1, Appli	C 177	14	1.4	50	2	US-08-316-439A-33	Sequence 33, Appl
105	15	1.5	1509	4	US-09-134-001C-761	Sequence 761, App	C 178	14	1.4	69	4	US-08-687-421-378	Sequence 378, App
106	15	1.5	1512	3	US-08-476-509B-1	Sequence 1, Appli	C 179	14	1.4	70	4	US-08-687-421-378	Sequence 383, App
107	15	1.5	1626	3	US-08-348-518C-1	Sequence 1, Appli	C 180	14	1.4	75	1	US-08-447-169A-89	Sequence 89, Appl
108	15	1.5	1762	1	US-07-870-029-1	Sequence 1, Appli	C 181	14	1.4	75	2	US-08-233-012C-89	Sequence 89, Appl
109	15	1.5	1882	1	US-09-091-725-14	Sequence 14, Appl	C 182	14	1.4	79	1	US-08-471-985A-107	Sequence 107, App
110	15	1.5	1969	1	US-08-106-761-3	Sequence 3, Appli	C 183	14	1.4	79	1	US-08-472-255A-163	Sequence 163, App
111	15	1.5	2125	4	US-09-232-160-2	Sequence 2, Appli	C 184	14	1.4	79	1	US-08-479-724A-163	Sequence 163, App
112	15	1.5	2187	4	US-09-134-001C-2131	Sequence 2131, Ap	C 185	14	1.4	79	3	US-08-472-256B-163	Sequence 163, App
113	15	1.5	2272	1	US-08-233-005-1	Sequence 1, Appli	C 186	14	1.4	79	4	US-08-952-793-163	Sequence 163, App
114	15	1.5	2272	1	US-08-428-943-1	Sequence 1, Appli	C 187	14	1.4	79	5	PCT-US95-12401A-107	Sequence 107, App
115	15	1.5	2272	3	US-09-016-649-1	Sequence 1, Appli	C 188	14	1.4	79	5	PCT-US96-09455A-163	Sequence 163, App
116	15	1.5	2272	5	PCT-US95-04858-1	Sequence 1, Appli	C 189	14	1.4	80	1	US-08-471-985A-86	Sequence 86, Appl
117	15	1.5	2357	4	US-09-149-476-262	Sequence 262, App	C 190	14	1.4	80	1	US-08-471-985A-88	Sequence 88, Appl
118	15	1.5	2361	4	US-09-011-197-1	Sequence 1, Appli	C 191	14	1.4	80	1	US-08-472-255A-132	Sequence 132, App
119	15	1.5	2404	4	US-08-945-771-1	Sequence 1, Appli	C 192	14	1.4	80	1	US-08-479-724A-132	Sequence 132, App
120	15	1.5	2514	1	US-09-149-476-261	Sequence 261, App	C 193	14	1.4	80	3	US-08-472-256B-132	Sequence 132, App
121	15	1.5	2515	1	US-08-061-465-3	Sequence 3, Appli	C 194	14	1.4	80	4	US-08-952-793-132	Sequence 132, App
122	15	1.5	2774	1	US-07-723-002C-5	Sequence 5, Appli	C 195	14	1.4	80	5	PCT-US95-12401A-86	Sequence 86, Appl
123	15	1.5	2811	1	US-08-040-548-31	Sequence 31, Appl	C 196	14	1.4	80	5	PCT-US95-12401A-88	Sequence 88, Appl
124	15	1.5	2811	1	US-08-466-344-31	Sequence 31, Appl	C 197	14	1.4	80	5	PCT-US96-09455A-132	Sequence 132, App
125	15	1.5	2817	6	5206152-6	Patent No. 5206152	C 198	14	1.4	81	4	US-08-687-421-379	Sequence 379, App
126	15	1.5	3487	4	US-09-453-702B-164	Sequence 164, App	C 199	14	1.4	81	4	US-08-687-421-380	Sequence 380, App
127	15	1.5	3549	4	US-09-381-862-1	Sequence 1, Appli	C 200	14	1.4	85	1	US-08-447-169A-201	Sequence 201, App
128	15	1.5	3827	2	US-08-447-031A-1	Sequence 1, Appli	C 201	14	1.4	86	1	US-08-447-169A-186	Sequence 186, App
129	15	1.5	3876	5	PCT-US95-17026-1	Sequence 1, Appli	C 202	14	1.4	89	4	US-09-133-321-8	Sequence 8, Appli
130	15	1.5	4163	4	US-09-004-838-70	Sequence 70, Appl	C 203	14	1.4	90	4	US-08-952-793-176	Sequence 176, App
131	15	1.5	4208	4	US-09-004-838-1	Sequence 1, Appli	C 204	14	1.4	90	5	PCT-US96-09455A-176	Sequence 176, App
132	15	1.5	4543	4	US-08-221-017B-1103	Sequence 1103, Ap	C 205	14	1.4	145	4	US-09-191-608-24	Sequence 24, Appl
133	15	1.5	4612	2	US-08-447-031A-8	Sequence 8, Appli	C 206	14	1.4	236	4	US-09-328-111-27	Sequence 27, Appl
134	15	1.5	4736	4	US-09-056-105-12	Sequence 12, Appl	C 207	14	1.4	236	4	US-09-328-111-108	Sequence 108, App
135	15	1.5	4833	4	US-09-066-047-1	Sequence 1, Appli	C 208	14	1.4	239	1	US-08-253-155A-50	Sequence 50, Appl
136	15	1.5	5857	4	US-09-293-170-4	Sequence 4, Appli	C 209	14	1.4	270	1	US-08-686-878A-31	Sequence 31, Appl
137	15	1.5	5857	4	US-09-293-170-4	Sequence 4, Appli	C 210	14	1.4	270	1	US-09-175-928-31	Sequence 31, Appl
138	15	1.5	6038	4	US-09-305-639-4	Sequence 4, Appli	C 211	14	1.4	301	4	US-09-605-785-263	Sequence 263, App
139	15	1.5	6519	1	US-08-588-985-1	Sequence 1, Appli	C 212	14	1.4	301	4	US-09-605-785-302	Sequence 302, App
140	15	1.5	6519	1	US-08-971-988-1	Sequence 1, Appli	C 213	14	1.4	301	4	US-09-439-313-263	Sequence 263, App
141	15	1.5	6822	4	US-09-426-998-3	Sequence 3, Appli	C 214	14	1.4	301	4	US-09-439-313-302	Sequence 302, App
142	15	1.5	6828	1	US-08-061-465-1	Sequence 1, Appli	C 215	14	1.4	301	4	US-09-352-616A-263	Sequence 263, App
143	15	1.5	7143	4	US-09-381-862-4	Sequence 4, Appli	C 216	14	1.4	301	4	US-09-352-616A-302	Sequence 302, App
144	15	1.5	7622	4	US-09-305-639-1	Sequence 1, Appli	C 217	14	1.4	301	4	US-09-232-149A-263	Sequence 263, App
145	15	1.5	7741	4	US-09-426-998-4	Sequence 4, Appli	C 218	14	1.4	301	4	US-09-232-149A-302	Sequence 302, App
146	15	1.5	8655	3	US-09-075-272-1	Sequence 1, Appli	C 219	14	1.4	305	1	US-08-062-472B-5	Sequence 5, Appli
147	15	1.5	9100	2	US-08-743-637B-27	Sequence 27, Appl	C 220	14	1.4	308	1	US-08-686-878A-40	Sequence 40, Appl
148	15	1.5	9100	3	US-08-526-840B-27	Sequence 27, Appl	C 221	14	1.4	308	1	US-09-175-928-40	Sequence 40, Appl
149	15	1.5	9936	4	US-08-972-927-2	Sequence 2, Appli	C 222	14	1.4	312	1	US-08-062-472B-4	Sequence 4, Appli
150	15	1.5	10917	3	US-08-926-842B-11	Sequence 11, Appl	C 223	14	1.4	318	4	US-09-134-001C-2436	Sequence 2436, Ap
151	15	1.5	12804	4	US-08-453-702B-149	Sequence 149, App	C 224	14	1.4	342	4	US-09-657-453A-18	Sequence 18, Appl
152	15	1.5	13206	4	US-08-961-527-33	Sequence 33, Appl	C 225	14	1.4	348	1	US-08-594-031-85	Sequence 85, Appl
153	15	1.5	15363	4	US-08-961-527-139	Sequence 139, App	C 226	14	1.4	350	3	US-08-888-077A-35	Sequence 35, Appl
154	15	1.5	17656	4	US-09-433-579-3	Sequence 3, Appli	C 227	14	1.4	369	4	US-09-422-487-5	Sequence 5, Appli
155	15	1.5	28001	4	US-09-819-993-3	Sequence 3, Appli	C 228	14	1.4	369	4	US-09-378-088A-127	Sequence 127, App
156	15	1.5	34185	4	US-09-545-481-3	Sequence 3, Appli	C 229	14	1.4	387	4	US-09-370-838-88	Sequence 88, Appl
157	15	1.5	40000	4	US-08-780-049-18	Sequence 18, Appl	C 230	14	1.4	389	4	US-08-943-731-73	Sequence 73, Appl
158	15	1.5	44377	2	US-08-804-227C-7	Sequence 7, Appli	C 231	14	1.4	400	4	US-08-976-259-37	Sequence 37, Appl
159	15	1.5	44377	2	US-08-804-198-1	Sequence 1, Appli	C 232	14	1.4	406	5	PCT-US91-06234A-4	Sequence 4, Appli
160	15	1.5	50341	2	US-08-247-901C-1	Sequence 1, Appli	C 233	14	1.4	417	1	US-08-470-179-117	Sequence 117, App
161	15	1.5	50341	2	US-09-075-904-1	Sequence 1, Appli	C 234	14	1.4	420	1	US-08-207-481-30	Sequence 30, Appl
162	15	1.5	52297	4	US-09-426-436-1	Sequence 1, Appli	C 235	14	1.4	420	5	PCT-US95-02689-32	Sequence 32, Appl
163	15	1.5	52297	4	US-08-705-557-1	Sequence 1, Appli	C 236	14	1.4	437	1	US-08-543-238-1	Sequence 1, Appli
164	15	1.5	65042	4	US-09-784-316-3	Sequence 3, Appli	C 237	14	1.4	437	1	US-08-420-526-1	Sequence 1, Appli
165	15	1.5	4403765	4	US-09-103-840A-2	Sequence 2, Appli	C 238	14	1.4	445	4	US-09-397-787-149	Sequence 149, App
166	15	1.5	4411529	4	US-09-103-840A-1	Sequence 1, Appli	C 239	14	1.4	447	2	US-08-911-445-10	Sequence 10, Appl
167	14	1.4	19	4	US-09-261-115-49	Sequence 49, Appl	C 240	14	1.4	447	2	US-09-182-983-10	Sequence 10, Appl
168	14	1.4	20	5	PCT-US95-02080-2	Sequence 2, Appli	C 241	14	1.4	471	2	US-08-465-380-11	Sequence 11, Appl
169	14	1.4	27	4	US-09-024-532-8	Sequence 8, Appli	C 242	14	1.4	471	2	US-08-480-478-40	Sequence 40, Appl
170	14	1.4	32	1	US-08-279-058B-46	Sequence 46, Appl	C 243	14	1.4	471	2	US-08-486-399-11	Sequence 11, Appl
171	14	1.4	41	3	US-08-828-323-46	Sequence 17, Appl	C 244	14	1.4	471	2	US-08-461-965-11	Sequence 11, Appl
172	14	1.4	42	1	US-08-270-314-17	Sequence 17, Appl	C 245	14	1.4	471	2	US-08-326-110A-40	Sequence 40, Appl
173	14	1.4	42	4	US-09-225-302-17	Sequence 17, Appl	C 246	14	1.4	471	2	US-08-326-110A-40	Sequence 40, Appl

247	1.4	14	Sequence 11, Appl	320	1.4	894	5	PCT-US95-14442A-90	Sequence 90, Appl
248	1.4	14	Sequence 11, Appl	321	1.4	895	4	US-09-280-116-87	Sequence 87, Appl
249	1.4	14	Sequence 11, Appl	322	1.4	910	4	US-09-221-017B-62	Sequence 62, Appl
250	1.4	14	Sequence 11, Appl	323	1.4	910	4	US-09-221-017B-62	Sequence 62, Appl
251	1.4	14	Sequence 11, Appl	324	1.4	911	4	US-09-457-046B-11	Sequence 11, Appl
252	1.4	14	Sequence 11, Appl	325	1.4	917	4	US-09-221-017B-678	Sequence 678, Appl
253	1.4	14	Sequence 11, Appl	326	1.4	944	4	US-09-386-493-4	Sequence 4, Appl
254	1.4	14	Sequence 351, Appl	327	1.4	973	4	US-08-936-165A-136	Sequence 136, Appl
255	1.4	14	Sequence 351, Appl	328	1.4	975	4	US-09-134-001C-528	Sequence 528, Appl
256	1.4	14	Sequence 351, Appl	329	1.4	981	4	US-09-134-001C-437	Sequence 437, Appl
257	1.4	14	Sequence 2, Appl	330	1.4	989	4	US-09-446-504-41	Sequence 41, Appl
258	1.4	14	Sequence 2, Appl	331	1.4	989	4	US-09-712-266-41	Sequence 41, Appl
259	1.4	14	Sequence 8, Appl	332	1.4	1001	4	US-09-641-638-360	Sequence 360, Appl
260	1.4	14	Sequence 2, Appl	333	1.4	1001	4	US-09-641-638-361	Sequence 361, Appl
261	1.4	14	Sequence 134, Appl	334	1.4	1001	4	US-09-641-638-362	Sequence 362, Appl
262	1.4	14	Sequence 11, Appl	335	1.4	1001	4	US-09-641-638-446	Sequence 446, Appl
263	1.4	14	Sequence 2678, Appl	336	1.4	1008	4	US-09-198-958A-9	Sequence 9, Appl
264	1.4	14	Sequence 99, Appl	337	1.4	1008	4	US-09-694-531-9	Sequence 9, Appl
265	1.4	14	Sequence 32, Appl	338	1.4	1029	1	US-08-096-182A-3	Sequence 3, Appl
266	1.4	14	Sequence 2099, Appl	339	1.4	1029	1	US-08-877-109-3	Sequence 3, Appl
267	1.4	14	Sequence 23, Appl	340	1.4	1029	3	US-08-798-760-3	Sequence 3, Appl
268	1.4	14	Sequence 83, Appl	341	1.4	1029	5	PCT-US94-08327-3	Sequence 3, Appl
269	1.4	14	Sequence 472, Appl	342	1.4	1029	6	5196333-1	Patent No. 5196333
270	1.4	14	Sequence 257, Appl	343	1.4	1032	1	US-08-553-633A-3	Sequence 3, Appl
271	1.4	14	Sequence 277, Appl	344	1.4	1036	4	US-09-004-838-3	Sequence 3, Appl
272	1.4	14	Sequence 42, Appl	345	1.4	1038	4	US-09-403-768-3	Sequence 3, Appl
273	1.4	14	Sequence 525, Appl	346	1.4	1073	4	US-09-347-803-5	Sequence 5, Appl
274	1.4	14	Sequence 179, Appl	347	1.4	1074	4	US-09-134-001C-382	Sequence 382, Appl
275	1.4	14	Sequence 415, Appl	348	1.4	1092	1	US-08-096-182A-5	Sequence 5, Appl
276	1.4	14	Sequence 286, Appl	349	1.4	1092	1	US-08-877-109-5	Sequence 5, Appl
277	1.4	14	Sequence 89, Appl	350	1.4	1092	3	US-08-798-760-5	Sequence 5, Appl
278	1.4	14	Sequence 89, Appl	351	1.4	1092	5	PCT-US94-08327-5	Sequence 5, Appl
279	1.4	14	Sequence 89, Appl	352	1.4	1093	4	US-09-348-265-1	Sequence 1, Appl
280	1.4	14	Sequence 38, Appl	353	1.4	1098	4	US-09-362-473-7	Sequence 7, Appl
281	1.4	14	Sequence 38, Appl	354	1.4	1100	4	US-07-861-458C-4	Sequence 4, Appl
282	1.4	14	Sequence 38, Appl	355	1.4	1104	1	US-08-307-499-57	Sequence 57, Appl
283	1.4	14	Sequence 1, Appl	356	1.4	1104	1	US-08-423-399B-36	Sequence 36, Appl
284	1.4	14	Sequence 1677, Appl	357	1.4	1104	2	US-09-299-268-57	Sequence 57, Appl
285	1.4	14	Sequence 1, Appl	358	1.4	1107	2	US-08-933-750C-77	Sequence 77, Appl
286	1.4	14	Sequence 375, Appl	359	1.4	1107	3	US-09-234-613-77	Sequence 77, Appl
287	1.4	14	Sequence 995, Appl	360	1.4	1121	1	US-08-433-783-45	Sequence 45, Appl
288	1.4	14	Sequence 2, Appl	361	1.4	1121	2	US-08-337-358-45	Sequence 45, Appl
289	1.4	14	Sequence 2, Appl	362	1.4	1121	5	PCT-US95-07537A-45	Sequence 45, Appl
290	1.4	14	Sequence 18, Appl	363	1.4	1121	5	PCT-US95-07537-45	Sequence 45, Appl
291	1.4	14	Sequence 28, Appl	364	1.4	1134	4	US-09-561-756-13	Sequence 13, Appl
292	1.4	14	Sequence 20, Appl	365	1.4	1134	4	US-09-227-721-13	Sequence 13, Appl
293	1.4	14	Sequence 19, Appl	366	1.4	1160	3	US-08-995-159-1	Sequence 1, Appl
294	1.4	14	Sequence 569, Appl	367	1.4	1162	2	US-08-423-399B-34	Sequence 34, Appl
295	1.4	14	Sequence 177, Appl	368	1.4	1162	2	US-08-332-562A-135	Sequence 135, Appl
296	1.4	14	Sequence 177, Appl	369	1.4	1168	4	US-08-961-527-362	Sequence 362, Appl
297	1.4	14	Sequence 177, Appl	370	1.4	1185	4	US-09-134-001C-1656	Sequence 1656, Appl
298	1.4	14	Sequence 455, Appl	371	1.4	1200	3	US-08-867-381A-1	Sequence 1, Appl
299	1.4	14	Sequence 101, Appl	372	1.4	1200	4	US-09-521-144-1	Sequence 1, Appl
300	1.4	14	Sequence 99, Appl	373	1.4	1206	4	US-09-191-608-21	Sequence 21, Appl
301	1.4	14	Sequence 101, Appl	374	1.4	1211	2	US-08-997-080-40	Sequence 40, Appl
302	1.4	14	Sequence 288, Appl	375	1.4	1211	2	US-08-997-362-40	Sequence 40, Appl
303	1.4	14	Sequence 1892, Appl	376	1.4	1211	3	US-08-873-970-40	Sequence 40, Appl
304	1.4	14	Sequence 15, Appl	377	1.4	1211	4	US-09-095-855-40	Sequence 40, Appl
305	1.4	14	Sequence 551, Appl	378	1.4	1211	4	US-08-705-347A-40	Sequence 40, Appl
306	1.4	14	Sequence 256, Appl	379	1.4	1211	4	US-09-324-542-40	Sequence 40, Appl
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308	1.4	14	Sequence 40, Appl	381	1.4	1211	4	US-09-200-643-40	Sequence 40, Appl
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312	1.4	14	Sequence 40, Appl	385	1.4	1248	4	US-09-105-537-7	Sequence 7, Appl
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315	1.4	14	Sequence 90, Appl	388	1.4	1260	1	US-08-436-074-52	Sequence 52, Appl
316	1.4	14	Sequence 817-795-90	389	1.4	1260	5	PCT-US96-06352-79	Sequence 79, Appl
317	1.4	14	Sequence 90, Appl	390	1.4	1260	5	PCT-US96-06583-79	Sequence 79, Appl
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394	1.4	1272	4	US-09-263-128-3	Sequence 3, Appli	467	14	1.4	1624	1	US-08-416-870C-5	Sequence 5, Appli
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422	1.4	1414	4	US-09-206-695-1	Sequence 1, Appli	495	14	1.4	1808	4	US-09-155-036-3	Sequence 3, Appli
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427	1.4	1452	1	US-08-553-058C-3	Sequence 3, Appli	c 500	14	1.4	1858	1	US-08-668-381A-6	Sequence 6, Appli
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569	14	1.4	2319	2	US-09-102-644-5	Sequence 5, Appli	642	14	1.4	3240	1	US-08-368-281-3	Sequence 3, Appli
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577	14	1.4	2427	4	US-09-134-001C-268	Sequence 268, App	c 650	14	1.4	3441	4	US-09-026-033-17	Sequence 17, Appli
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582	14	1.4	2598	4	US-09-026-033-18	Sequence 18, Appli	c 655	14	1.4	3498	4	US-09-350-982C-4	Sequence 4, Appli
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585	14	1.4	2601	2	US-09-060-692-53	Sequence 53, Appli	c 658	14	1.4	3565	4	US-09-749-588-1	Sequence 1, Appli
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C 842	14	1.4	10299	2	US-08-477-451-5	Sequence 1, Appl	C 915	14	1.4	87350	3	US-08-781-891-79	Sequence 79, Appl
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C 850	14	1.4	12286	4	US-09-357-206A-1	Patent No. 5206163	C 923	13	1.3	20	4	US-09-710-200-28	Sequence 28, Appl
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C 854	14	1.4	12793	4	US-09-004-838-124	Sequence 124, App	927	13	1.3	21	4	US-09-338-907-63	Sequence 63, Appl
C 855	14	1.4	12949	4	US-09-538-414-11	Sequence 11, Appl	928	13	1.3	21	4	US-09-218-207-63	Sequence 63, Appl
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C 872	14	1.4	19307	4	US-09-427-048A-10	Sequence 10, Appl	C 945	13	1.3	31	4	US-09-022-765-28	Sequence 28, Appl
C 873	14	1.4	19446	4	US-08-961-527-51	Sequence 51, Appl	C 946	13	1.3	31	4	US-09-510-925A-1	Sequence 1, Appl
C 874	14	1.4	19702	4	US-08-961-527-7	Sequence 7, Appl	C 947	13	1.3	33	4	US-09-238-356-33	Sequence 33, Appl
C 875	14	1.4	19932	2	US-08-477-451-25	Sequence 25, Appl	C 948	13	1.3	34	2	US-08-846-762-40	Sequence 40, Appl
C 876	14	1.4	20199	4	US-08-961-527-6	Sequence 6, Appl	C 949	13	1.3	34	3	US-09-133-914-1	Sequence 1, Appl
C 877	14	1.4	25165	4	US-09-453-702B-39	Sequence 39, Appl	C 950	13	1.3	34	4	US-09-469-197-1	Sequence 1, Appl
C 878	14	1.4	26764	1	US-08-370-975B-1	Sequence 1, Appl	C 951	13	1.3	36	2	US-08-816-158B-30	Sequence 30, Appl
C 879	14	1.4	28882	4	US-08-961-527-140	Sequence 140, App	C 952	13	1.3	36	3	US-08-815-809-15	Sequence 15, Appl
C 880	14	1.4	31328	4	US-09-215-694-19	Sequence 19, Appl	C 953	13	1.3	36	3	US-09-079-587-30	Sequence 30, Appl
C 881	14	1.4	31960	4	US-09-453-702B-11	Sequence 11, Appl	C 954	13	1.3	36	3	US-08-961-083-419	Sequence 419, App
C 882	14	1.4	36159	4	US-09-749-588-3	Sequence 3, Appl	C 955	13	1.3	36	4	US-08-482-918-17	Sequence 17, Appl
C 883	14	1.4	37895	1	US-08-375-709-1	Sequence 1, Appl	C 956	13	1.3	36	4	US-09-224-681-17	Sequence 17, Appl
C 884	14	1.4	37895	1	US-08-752-929-1	Sequence 1, Appl	C 957	13	1.3	36	4	US-08-336-728A-17	Sequence 17, Appl
C 885	14	1.4	37895	3	US-09-090-793-1	Sequence 1, Appl	C 958	13	1.3	37	2	US-08-898-560-4	Sequence 4, Appl
C 886	14	1.4	37948	4	US-09-251-645-11	Sequence 11, Appl	C 959	13	1.3	37	2	US-08-898-560-5	Sequence 5, Appl
C 887	14	1.4	38584	4	US-09-453-702B-50	Sequence 50, Appl	960	13	1.3	37	4	US-09-518-914-34	Sequence 34, Appl
C 888	14	1.4	38682	4	US-08-943-731-2	Sequence 3, Appl	961	13	1.3	38	1	US-08-373-124A-609	Sequence 609, App
C 889	14	1.4	43950	4	US-09-735-934A-3	Sequence 3, Appl	962	13	1.3	38	1	US-08-435-628-609	Sequence 609, App
C 890	14	1.4	45716	4	US-08-965-048-5	Sequence 5, Appl	C 963	13	1.3	38	1	US-08-435-628-1650	Sequence 1650, App
C 891	14	1.4	45989	4	US-08-965-048-6	Sequence 6, Appl	964	13	1.3	38	4	US-09-110-517-15	Sequence 15, Appl
C 892	14	1.4	46899	1	US-08-471-119A-1	Sequence 1, Appl	965	13	1.3	39	2	US-08-951-871-25	Sequence 25, Appl
C 893	14	1.4	48908	4	US-09-453-702B-137	Sequence 137, App	966	13	1.3	42	4	US-09-498-959-5	Sequence 5, Appl
C 894	14	1.4	48974	4	US-08-920-422-17	Sequence 17, Appl	C 967	13	1.3	44	2	US-08-875-154-28	Sequence 28, Appl
C 895	14	1.4	50000	4	US-09-146-053-4	Sequence 4, Appl	C 968	13	1.3	44	4	US-09-538-709-1147	Sequence 1147, App
C 896	14	1.4	51952	3	US-08-947-823-1	Sequence 1, Appl	969	13	1.3	49	4	US-09-345-882-6	Sequence 6, Appl
C 897	14	1.4	59065	4	US-09-813-817-3	Sequence 3, Appl	970	13	1.3	55	1	US-07-910-760-3	Sequence 3, Appl
C 898	14	1.4	61663	4	US-09-978-197-3	Sequence 3, Appl	971	13	1.3	56	1	US-08-440-519-3	Sequence 3, Appl
C 899	14	1.4	65042	4	US-09-453-702B-62	Sequence 62, Appl	972	13	1.3	56	3	US-08-444-818-241	Sequence 241, App
C 900	14	1.4	68750	3	US-09-784-316-3	Sequence 3, Appl	973	13	1.3	56	3	US-08-440-549-3	Sequence 3, Appl
C 901	14	1.4	68750	4	US-09-335-409-1	Sequence 1, Appl	C 974	13	1.3	56	5	PCT-US91-02225-3	Sequence 3, Appl
C 902	14	1.4	68750	4	US-09-568-102-1	Sequence 1, Appl	975	13	1.3	60	4	US-08-654-737B-8	Sequence 8, Appl
C 903	14	1.4	68750	4	US-09-567-969-1	Sequence 1, Appl	976	13	1.3	60	4	US-08-899-279-38	Sequence 38, Appl

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-207

Query Match 1.9%; Score 18; DB 3; Length 29604;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 CAAAAATGCCAACATTA 328
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DB 9553 CAAAAATGCCAACATTA 9536

RESULT 4
US-08-248-474-44
Sequence 44, Application US/08248474
Patent No. 5612471
GENERAL INFORMATION:
APPLICANT: MCK. BIRD, David
APPLICANT: WILSON, Mark A.
TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,474
FILING DATE: 25-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..193
OTHER INFORMATION: /standard_name= "DB# 168"
US-08-248-474-44

Query Match 1.7%; Score 17; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 GATTCGGGTGCTCT 578
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DB 85 GATTCGGGTGCTCT 101

RESULT 5
US-08-756-849-44
Sequence 44, Application US/08756849
Patent No. 6093810
GENERAL INFORMATION:
APPLICANT: Bird, David MCK.
APPLICANT: Wilson, Mark A.
TITLE OF INVENTION: Nematode-Induced Genes in Tomato
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,849
FILING DATE: 26-NOV-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,474
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-053510US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..193
OTHER INFORMATION: /standard_name= "DB# 168"
US-08-756-849-44

Query Match 1.7%; Score 17; DB 3; Length 193;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 562 GATTGGGTGCTGT 578
Db 85 GATTGGGTGCTGT 101
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RESULT 6

US-09-315-794-61
; Sequence 61, Application US/09315794
; Patent No. 6197517
; GENERAL INFORMATION:
; APPLICANT: Roberts, Christopher J.
; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
; FILE REFERENCE: 9301-053
; CURRENT APPLICATION NUMBER: US/09/315,794
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 61
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-315-794-61

Query Match 1.7%; Score 17; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 825 TGAACAAATGCTATAA 841
Db 15 TGAACAAATGCTATAA 31
|||||

RESULT 7

US-09-389-341-61
; Sequence 61, Application US/09389341
; Patent No. 6200803
; GENERAL INFORMATION:
; APPLICANT: Roberts, Christopher J.
; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATIVE
; FILE REFERENCE: 9301-057
; CURRENT APPLICATION NUMBER: US/09/389,341
; CURRENT FILING DATE: 1999-09-02
; EARLIER APPLICATION NUMBER: 09/315,794
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 61
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-389-341-61

Query Match 1.7%; Score 17; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 825 TGAACAAATGCTATAA 841
Db 15 TGAACAAATGCTATAA 31
|||||

RESULT 8

US-09-173-300-16/c
; Sequence 16, Application US/09173300
; Patent No. 6451581
; GENERAL INFORMATION:

; APPLICANT: Falco, Saverio Carl
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1126
; CURRENT APPLICATION NUMBER: US/09/173,300
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 60/063,423
; EARLIER FILING DATE: 1997 October 28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 16
; LENGTH: 965
; TYPE: DNA
; ORGANISM: Glycine max
US-09-173-300-16

Query Match 1.7%; Score 17; DB 4; Length 965;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 284 ATGGCAAAACAAGGATG 300
Db 17 ATGGCAAAACAAGGATG 1
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RESULT 9

US-09-134-001C-1491
; Sequence 1491, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1491
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1491

Query Match 1.7%; Score 17; DB 4; Length 993;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 688 GCTGCTTACGATATCAT 704
Db 700 GCTGCTTACGATATCAT 716
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RESULT 10

US-08-136-743B-1/c
; Sequence 1, Application US/08136743B
; Patent No. 5459063
; GENERAL INFORMATION:
; APPLICANT: Barry S. Cooperman, Harvey Rubin,
; APPLICANT: Jerome Salem, and Alison L. Fisher
; TITLE OF INVENTION: "plasmodium falciparum Ribonu-
; TITLE OF INVENTION: cleotide reductase, DNA Sequences Therefor and Peptide Inhibi-
; TITLE OF INVENTION: Thereof"
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The University of Pennsylvania
; STREET: Suite 330

STREET: 3700 Market Street
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19104-3246
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,743B
FILING DATE: 10/14/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3957-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5459063e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-136-743B-1

Query Match 1.7%; Score 17; DB 1; Length 1112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 CTTGCTGCAAAAATGC 320
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Db 272 CTTGCTGCAAAAATGC 256

RESULT 11
US-08-869-506-1
Sequence 1, Application US/08869506
Patent No. 5827710
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
APPLICANT: Fujita, Tutosi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5827710th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,506
FILING DATE: 05-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 55..1053
US-08-869-506-1

Query Match 1.7%; Score 17; DB 1; Length 1240;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 550 GGAGAACATGGTGATTC 566
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Db 625 GGAGAACATGGTGATTC 641

RESULT 12
US-09-128-967-1
Sequence 1, Application US/09128967
Patent No. 6057141
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
APPLICANT: Fujita, Tutosi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 6057141th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/869,506
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 55...1053
US-09-128-967-1

Query Match      1.7%; Score 17; DB 3; Length 1240;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 550 GGAGAACATGCTGATTC 566
Db 625 GGAGAACATGCTGATTC 641

RESULT 13
US-09-234-186-2
; Sequence 2, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-2

Query Match      1.7%; Score 17; DB 4; Length 1315;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 914 AATTGATGGAATAATCA 930
Db 201 AATTGATGGAATAATCA 217

RESULT 14
US-09-234-186-4
; Sequence 4, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
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; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)...(846)
US-09-234-186-4

Query Match      1.7%; Score 17; DB 4; Length 1315;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 914 AATTGATGGAATAATCA 930
Db 201 AATTGATGGAATAATCA 217

RESULT 15
US-09-234-186-5
; Sequence 5, Application US/09234186
; Patent No. 6312947
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 01997/201005
; CURRENT APPLICATION NUMBER: US/09/234,186
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: 07/898,933
; EARLIER FILING DATE: 1992-06-12
; EARLIER APPLICATION NUMBER: 07/927,681
; EARLIER FILING DATE: 1992-08-10
; EARLIER APPLICATION NUMBER: 08/288,295
; EARLIER FILING DATE: 1994-08-10
; EARLIER APPLICATION NUMBER: 08/801,248
; EARLIER FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
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US-09-234-186-5

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Search completed: July 31, 2003, 12:44:40
Job time : 98 secs
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 11:59:02 ; Search time 260 Seconds
(without alignments)
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Title: US-09-992-430B-21

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Searched: 1439767 seqs, 1031500376 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	2.0	1146	15	US-10-027-632-124906
5	19	2.0	1755	11	US-09-731-872-15
6	19	2.0	1759	11	US-09-731-872-15
7	19	2.0	2352	15	US-10-128-714-87
8	19	2.0	2352	15	US-10-128-714-87
9	19	2.0	3144	15	US-10-274-266-3
10	18	1.9	492	12	US-09-918-995-11651
11	18	1.9	559	15	US-10-027-632-233560
12	18	1.9	828	11	US-09-974-300-6602
13	18	1.9	986	11	US-09-938-842A-4346
14	18	1.9	996	11	US-09-938-842A-4346
15	18	1.9	2338	15	US-10-027-632-259728
16	18	1.9	2338	15	US-10-027-632-259729

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1.7	329	11	US-09-783-590-1290	Sequence 1290, Ap
1.7	344	10	US-09-777-584-756	Sequence 756, App
1.7	344	10	US-09-777-564-1494	Sequence 1494, Ap
1.7	344	15	US-10-015-219-756	Sequence 756, App
1.7	344	15	US-10-015-219-1494	Sequence 1494, Ap
1.7	377	11	US-09-983-965-5432	Sequence 5432, Ap
1.7	422	12	US-09-918-995-5225	Sequence 5225, Ap
1.7	432	11	US-09-783-590-6454	Sequence 6454, Ap
1.7	487	12	US-09-918-995-12259	Sequence 12259, A
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1.7	598	15	US-10-027-632-300434	Sequence 300434,
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1.7	640	15	US-10-027-632-113106	Sequence 113106,
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1.7	971	15	US-10-027-632-121628	Sequence 121628,
1.7	971	15	US-10-027-632-121629	Sequence 121629,
1.7	971	15	US-10-027-632-121630	Sequence 121630,
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1.7	1892	11	US-09-917-800A-1716	Sequence 1716, Ap
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1.7	3172	15	US-10-013-477-6	Sequence 6, Appli
1.7	3799	10	US-09-866-562-24	Sequence 24, Appl
1.7	3799	11	US-09-960-253-161	Sequence 161, App
1.7	4082	11	US-09-864-864-325	Sequence 325, App
1.7	4240	12	US-09-919-039-208	Sequence 208, App
1.7	6765	15	US-10-037-270-481	Sequence 481, App
1.7	14962	10	US-09-764-878-244	Sequence 244, App
1.7	14962	15	US-10-079-854-244	Sequence 244, App
1.7	20099	15	US-10-177-744A-12	Sequence 12, Appl
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1.7	21727	11	US-09-764-864-1604	Sequence 1604, Ap
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1.6	129	15	US-10-300-285-8	Sequence 8, Appli
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1.6	265	11	US-09-878-574-453	Sequence 453, App
1.6	295	11	US-09-796-692-4124	Sequence 4124, Ap
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1.6	359	11	US-09-878-574-3321	Sequence 3321, Ap
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1.6	409	15	US-10-040-862-9430	Sequence 9430, Ap
1.6	418	11	US-09-983-965-5780	Sequence 5780, Ap
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c 91	16	1.6	446	15	US-10-171-581-315	Sequence 315, App	164	16	1.6	878	15	US-10-027-632-122083	Sequence 122083, App
c 92	16	1.6	450	11	US-09-925-300-939	Sequence 939, App	165	16	1.6	960	10	US-09-939-980-46	Sequence 46, Appl
c 93	16	1.6	452	15	US-10-040-739-1119	Sequence 1119, App	166	16	1.6	978	12	US-09-991-936-18	Sequence 18, Appl
c 94	16	1.6	462	10	US-09-864-761-14088	Sequence 14088, A	167	16	1.6	978	12	US-09-991-936-18	Sequence 18, Appl
c 95	16	1.6	464	12	US-09-918-995-15685	Sequence 15685, A	168	16	1.6	987	10	US-09-815-242-9774	Sequence 9774, App
c 96	16	1.6	474	15	US-10-027-632-192630	Sequence 192630, App	169	16	1.6	990	15	US-10-027-632-192630	Sequence 192630, App
c 97	16	1.6	482	12	US-09-918-995-12096	Sequence 12096, A	170	16	1.6	1036	11	US-09-925-300-713	Sequence 713, App
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c 102	16	1.6	488	15	US-10-027-632-290017	Sequence 290017, App	175	16	1.6	1219	15	US-10-027-632-241194	Sequence 241194, App
c 103	16	1.6	492	12	US-10-027-632-38029	Sequence 38029, A	176	16	1.6	1239	10	US-09-815-242-7880	Sequence 7880, App
c 104	16	1.6	492	12	US-09-918-995-30493	Sequence 30493, A	177	16	1.6	1239	11	US-09-974-300-674	Sequence 674, App
c 105	16	1.6	495	12	US-09-764-891-6606	Sequence 6606, App	178	16	1.6	1239	11	US-09-974-300-674	Sequence 674, App
c 106	16	1.6	495	15	US-10-027-632-215369	Sequence 215369, App	179	16	1.6	1345	10	US-09-864-761-19745	Sequence 19745, A
c 107	16	1.6	525	15	US-10-091-572-470	Sequence 470, App	180	16	1.6	1371	11	US-09-801-368-203	Sequence 203, App
c 108	16	1.6	525	15	US-10-027-632-84506	Sequence 84506, A	181	16	1.6	1476	11	US-09-801-368-203	Sequence 203, App
c 109	16	1.6	527	11	US-09-833-381-1083	Sequence 1083, App	182	16	1.6	1484	11	US-09-764-868-429	Sequence 429, App
c 110	16	1.6	528	15	US-10-060-036-3382	Sequence 3382, App	183	16	1.6	1521	12	US-09-984-827-12	Sequence 12, Appl
c 111	16	1.6	546	15	US-10-027-632-180787	Sequence 180787, App	184	16	1.6	1536	12	US-09-918-624B-37	Sequence 37, Appl
c 112	16	1.6	554	10	US-09-864-761-13363	Sequence 13363, A	185	16	1.6	1536	12	US-09-918-624B-37	Sequence 37, Appl
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c 114	16	1.6	560	15	US-10-027-632-321524	Sequence 321524, App	187	16	1.6	1714	12	US-09-991-936-13	Sequence 13, Appl
c 115	16	1.6	560	15	US-10-027-632-48210	Sequence 48210, A	188	16	1.6	1788	10	US-09-991-936-15	Sequence 15, Appl
c 116	16	1.6	560	15	US-10-027-632-48211	Sequence 48211, A	189	16	1.6	1815	10	US-09-815-242-4189	Sequence 4189, App
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c 126	16	1.6	603	15	US-10-027-632-227134	Sequence 227134, App	199	16	1.6	2147	11	US-09-764-855-326	Sequence 326, App
c 127	16	1.6	603	15	US-10-027-632-227135	Sequence 227135, App	200	16	1.6	2147	11	US-10-073-349-326	Sequence 326, App
c 128	16	1.6	611	15	US-10-027-632-203536	Sequence 203536, App	201	16	1.6	2190	15	US-10-027-632-261915	Sequence 261915, App
c 129	16	1.6	615	15	US-10-027-632-238921	Sequence 238921, App	202	16	1.6	2236	12	US-09-764-891-6383	Sequence 6383, App
c 130	16	1.6	618	15	US-10-027-632-198651	Sequence 198651, App	203	16	1.6	2236	12	US-10-205-428-673	Sequence 673, App
c 131	16	1.6	623	15	US-10-119-926-88	Sequence 88, Appl	204	16	1.6	2266	11	US-09-764-864-17	Sequence 17, Appl
c 132	16	1.6	624	15	US-10-027-632-228376	Sequence 228376, App	205	16	1.6	2268	10	US-09-815-242-6058	Sequence 6058, App
c 133	16	1.6	624	15	US-10-027-632-228377	Sequence 228377, App	206	16	1.6	2344	15	US-10-024-632-1	Sequence 1, Appl
c 134	16	1.6	626	15	US-10-027-632-114107	Sequence 114107, App	207	16	1.6	2344	15	US-09-349-015-31	Sequence 31, Appl
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c 136	16	1.6	634	15	US-10-027-632-252572	Sequence 252572, App	209	16	1.6	2702	11	US-09-834-975-837	Sequence 837, App
c 137	16	1.6	637	15	US-10-027-632-195859	Sequence 195859, App	210	16	1.6	2790	15	US-10-072-094-98	Sequence 98, App
c 138	16	1.6	642	15	US-10-027-632-20926	Sequence 20926, App	211	16	1.6	2844	15	US-10-044-090-813	Sequence 813, App
c 139	16	1.6	645	12	US-09-764-891-6671	Sequence 6671, App	212	16	1.6	2890	15	US-10-027-632-256651	Sequence 256651, App
c 140	16	1.6	645	15	US-09-764-891-6674	Sequence 6674, App	213	16	1.6	2991	15	US-10-201-386-48	Sequence 48, Appl
c 141	16	1.6	645	15	US-10-091-572-532	Sequence 532, App	214	16	1.6	3168	15	US-10-027-632-114963	Sequence 114963, App
c 142	16	1.6	645	15	US-10-091-572-535	Sequence 535, App	215	16	1.6	3168	15	US-10-173-539-7	Sequence 7, Appl
c 143	16	1.6	647	15	US-10-027-632-44349	Sequence 44349, App	216	16	1.6	3367	15	US-10-198-846-9722	Sequence 9722, App
c 144	16	1.6	647	15	US-10-027-632-244428	Sequence 244428, App	217	16	1.6	3368	15	US-10-198-846-9722	Sequence 9722, App
c 145	16	1.6	647	15	US-10-027-632-244429	Sequence 244429, App	218	16	1.6	3368	15	US-10-173-539-3	Sequence 3, Appl
c 146	16	1.6	661	15	US-10-027-632-287226	Sequence 287226, App	219	16	1.6	3368	15	US-10-173-539-3	Sequence 3, Appl
c 147	16	1.6	661	15	US-10-027-632-287227	Sequence 287227, App	220	16	1.6	3368	15	US-10-173-539-3	Sequence 3, Appl
c 148	16	1.6	666	15	US-10-027-632-270003	Sequence 270003, App	221	16	1.6	3368	15	US-10-173-539-3	Sequence 3, Appl
c 149	16	1.6	676	15	US-10-027-632-205278	Sequence 205278, App	222	16	1.6	3368	15	US-10-173-539-3	Sequence 3, Appl
c 150	16	1.6	697	15	US-10-027-632-286967	Sequence 286967, App	223	16	1.6	3415	15	US-10-125-772-7	Sequence 7, Appl
c 151	16	1.6	702	15	US-10-071-766-40	Sequence 40, Appl	224	16	1.6	3415	15	US-10-125-772-7	Sequence 7, Appl
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c 154	16	1.6	715	15	US-10-027-632-28355	Sequence 28355, A	227	16	1.6	4031	15	US-10-125-772-9	Sequence 9, Appl
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c 157	16	1.6	755	15	US-10-027-632-148827	Sequence 148827, App	230	16	1.6	4302	11	US-09-801-368-59	Sequence 59, Appl
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c 160	16	1.6	818	15	US-10-027-632-167384	Sequence 167384, App	233	16	1.6	6551	11	US-09-954-456-178	Sequence 178, App
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c 162	16	1.6	825	11	US-09-738-626-994	Sequence 994, App	235	16	1.6	6763	15	US-10-176-847-55	Sequence 55, Appl

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c 238	16	1.6	10236	15	US-10-114-170-240	Sequence 240, App	c 311	15	1.5	375	10	US-09-923-779-117	Sequence 117, App
c 239	16	1.6	15231	11	US-09-917-800A-1505	Sequence 1505, Ap	c 312	15	1.5	375	10	US-09-923-779-128	Sequence 128, App
c 240	16	1.6	15366	10	US-09-764-860-1057	Sequence 1057, Ap	c 313	15	1.5	375	10	US-09-923-779-129	Sequence 129, App
c 241	16	1.6	15366	15	US-10-074-095-1057	Sequence 1057, Ap	c 314	15	1.5	375	10	US-09-923-779-141	Sequence 141, App
c 242	16	1.6	18449	11	US-09-764-868-1457	Sequence 1457, Ap	c 315	15	1.5	377	11	US-09-954-456-232	Sequence 232, App
c 243	16	1.6	21423	11	US-09-764-877-2835	Sequence 2835, Ap	c 316	15	1.5	377	11	US-10-027-632-253326	Sequence 253326,
c 244	16	1.6	31208	10	US-09-852-067-3	Sequence 3, Appl	c 317	15	1.5	385	11	US-09-878-574-760	Sequence 760, App
c 245	16	1.6	31208	15	US-10-338-691-3	Sequence 3, Appl	c 318	15	1.5	387	12	US-09-764-891-8049	Sequence 8049, Ap
c 246	16	1.6	32190	15	US-09-764-878-201	Sequence 201, App	c 319	15	1.5	387	12	US-09-764-891-8050	Sequence 8050, Ap
c 247	16	1.6	32190	15	US-10-079-854-201	Sequence 201, App	c 320	15	1.5	387	12	US-09-764-891-8051	Sequence 8051, Ap
c 248	16	1.6	32193	10	US-09-764-878-200	Sequence 200, App	c 321	15	1.5	396	10	US-09-825-294-138	Sequence 138, App
c 249	16	1.6	32193	15	US-10-079-854-200	Sequence 200, App	c 322	15	1.5	396	11	US-09-970-966-138	Sequence 138, App
c 250	16	1.6	32249	10	US-09-764-878-202	Sequence 202, App	c 323	15	1.5	396	14	US-10-212-677-138	Sequence 138, App
c 251	16	1.6	32249	15	US-10-079-854-202	Sequence 202, App	c 324	15	1.5	400	8	US-08-781-986A-1502	Sequence 1502, Ap
c 252	16	1.6	43058	11	US-09-954-456-292	Sequence 292, App	c 325	15	1.5	400	8	US-08-781-986A-1502	Sequence 1502, Ap
c 253	16	1.6	43058	11	US-09-954-456-529	Sequence 529, App	c 326	15	1.5	401	10	US-09-922-217-45	Sequence 45, Appl
c 254	16	1.6	43058	11	US-09-880-107-3950	Sequence 3950, Ap	c 327	15	1.5	401	11	US-09-833-263-45	Sequence 45, Appl
c 255	16	1.6	55795	11	US-09-880-107-3950	Sequence 3950, Ap	c 328	15	1.5	401	11	US-10-025-380-45	Sequence 45, Appl
c 256	16	1.6	145831	11	US-09-969-708-79	Sequence 79, Appl	c 329	15	1.5	405	11	US-09-560-863-492	Sequence 492, App
c 257	16	1.6	145831	11	US-09-954-456-2116	Sequence 2116, Ap	c 330	15	1.5	405	11	US-10-027-632-140856	Sequence 140856,
c 258	16	1.6	402850	12	US-09-844-653-5	Sequence 5, Appl	c 331	15	1.5	408	15	US-10-198-846-12667	Sequence 12667, A
c 259	16	1.6	1503841	10	US-09-795-668-1	Sequence 1, Appl	c 332	15	1.5	410	11	US-09-960-352-4202	Sequence 4202, Ap
c 260	16	1.6	1503841	10	US-09-795-668-1	Sequence 1, Appl	c 333	15	1.5	410	11	US-09-960-352-4202	Sequence 4202, Ap
c 261	16	1.6	1503841	11	US-09-946-807-1	Sequence 1, Appl	c 334	15	1.5	418	10	US-09-962-436-220	Sequence 220, App
c 262	16	1.6	1691139	15	US-10-067-514-1	Sequence 1, Appl	c 335	15	1.5	418	12	US-09-918-995-1055	Sequence 1055, Ap
c 263	16	1.6	3309400	11	US-09-738-626-1	Sequence 1, Appl	c 336	15	1.5	420	12	US-09-991-936-362	Sequence 362, App
c 264	15	1.5	24	11	US-09-798-584-10	Sequence 10, Appl	c 337	15	1.5	420	15	US-10-027-632-183086	Sequence 183086,
c 265	15	1.5	25	15	US-10-098-263B-89065	Sequence 10, Appl	c 338	15	1.5	422	12	US-09-918-995-8357	Sequence 8357, Ap
c 266	15	1.5	39	15	US-10-118-079-16	Sequence 16, Appl	c 339	15	1.5	425	15	US-10-027-632-183752	Sequence 183752,
c 267	15	1.5	45	12	US-09-940-244-158	Sequence 158, App	c 340	15	1.5	428	11	US-09-960-352-601	Sequence 601, App
c 268	15	1.5	45	12	US-09-864-636A-592	Sequence 592, App	c 341	15	1.5	430	10	US-09-864-761-14096	Sequence 14096, A
c 269	15	1.5	45	15	US-10-033-297-158	Sequence 158, App	c 342	15	1.5	430	12	US-09-918-995-32630	Sequence 32630, A
c 270	15	1.5	155	11	US-09-764-877-879	Sequence 879, App	c 343	15	1.5	436	10	US-09-918-686-24	Sequence 24, Appl
c 271	15	1.5	173	11	US-09-736-457-503	Sequence 503, App	c 344	15	1.5	439	11	US-09-960-352-3931	Sequence 3931, Ap
c 272	15	1.5	173	11	US-09-902-941-503	Sequence 503, App	c 345	15	1.5	440	15	US-10-027-632-42837	Sequence 42837, A
c 273	15	1.5	173	11	US-09-849-626-503	Sequence 503, App	c 346	15	1.5	446	15	US-10-027-632-62097	Sequence 62097, A
c 274	15	1.5	173	12	US-09-476-300-503	Sequence 503, App	c 347	15	1.5	446	15	US-10-027-632-63418	Sequence 63418, A
c 275	15	1.5	173	15	US-10-017-754-503	Sequence 503, App	c 348	15	1.5	447	11	US-10-027-632-297939	Sequence 297939,
c 276	15	1.5	188	10	US-09-912-020-77	Sequence 77, Appl	c 349	15	1.5	450	12	US-09-738-626-2797	Sequence 2797, Ap
c 277	15	1.5	188	10	US-09-912-020-481	Sequence 481, App	c 350	15	1.5	450	12	US-09-918-995-45578	Sequence 45578, A
c 278	15	1.5	211	11	US-09-983-965-5235	Sequence 5235, Ap	c 351	15	1.5	454	15	US-10-027-632-87288	Sequence 87288, A
c 279	15	1.5	214	11	US-09-960-352-8594	Sequence 8594, Ap	c 352	15	1.5	454	15	US-10-027-632-182405	Sequence 182405,
c 280	15	1.5	215	10	US-09-923-876-4635	Sequence 4635, Ap	c 353	15	1.5	455	11	US-09-922-217-383	Sequence 383, App
c 281	15	1.5	232	10	US-09-923-876-3597	Sequence 3597, Ap	c 354	15	1.5	455	11	US-09-833-263-383	Sequence 383, App
c 282	15	1.5	233	11	US-09-878-574-7773	Sequence 7773, Ap	c 355	15	1.5	455	15	US-10-025-380-383	Sequence 383, App
c 283	15	1.5	245	15	US-10-027-632-275440	Sequence 275440,	c 356	15	1.5	455	15	US-10-027-632-181018	Sequence 181018,
c 284	15	1.5	247	11	US-09-878-574-10727	Sequence 10727, A	c 357	15	1.5	456	10	US-09-864-761-14332	Sequence 14332, A
c 285	15	1.5	258	11	US-09-878-574-12810	Sequence 12810, A	c 358	15	1.5	457	11	US-09-918-995-27800	Sequence 27800, A
c 286	15	1.5	267	12	US-09-803-719-1647	Sequence 1647, Ap	c 359	15	1.5	461	12	US-09-983-965-178	Sequence 178, App
c 287	15	1.5	269	10	US-09-294-093B-3909	Sequence 3909, Ap	c 360	15	1.5	461	15	US-09-918-995-2358	Sequence 2358, Ap
c 288	15	1.5	275	11	US-09-878-574-14072	Sequence 14072, A	c 361	15	1.5	462	12	US-10-027-632-274412	Sequence 274412,
c 289	15	1.5	276	11	US-09-738-626-2854	Sequence 2854, Ap	c 362	15	1.5	462	12	US-09-918-995-32802	Sequence 32802, A
c 290	15	1.5	284	12	US-09-232-785-244	Sequence 244, App	c 363	15	1.5	463	15	US-10-027-632-183930	Sequence 183930,
c 291	15	1.5	287	10	US-09-294-093B-3148	Sequence 3148, App	c 364	15	1.5	463	15	US-10-027-632-183931	Sequence 183931,
c 292	15	1.5	302	11	US-09-960-352-2799	Sequence 2799, Ap	c 365	15	1.5	464	15	US-10-027-632-269826	Sequence 269826,
c 293	15	1.5	303	10	US-09-741-669-130	Sequence 130, App	c 366	15	1.5	464	15	US-10-027-632-269827	Sequence 269827,
c 294	15	1.5	303	10	US-09-912-020-230	Sequence 230, App	c 367	15	1.5	467	11	US-09-920-300A-911	Sequence 911, App
c 295	15	1.5	303	10	US-09-815-242-6260	Sequence 6260, Ap	c 368	15	1.5	467	15	US-10-033-528-911	Sequence 911, App
c 296	15	1.5	309	11	US-09-880-107-452	Sequence 452, App	c 369	15	1.5	467	15	US-10-027-632-274411	Sequence 274411,
c 297	15	1.5	321	12	US-09-764-891-1541	Sequence 1541, Ap	c 370	15	1.5	467	15	US-10-027-632-274413	Sequence 274413,
c 298	15	1.5	345	12	US-09-910-082A-28	Sequence 28, Appl	c 371	15	1.5	468	10	US-09-867-550-1295	Sequence 1295, Ap
c 299	15	1.5	351	10	US-09-745-288-77	Sequence 77, Appl	c 372	15	1.5	470	10	US-09-864-761-3101	Sequence 3101, Ap
c 300	15	1.5	351	11	US-09-974-300-3760	Sequence 3760, Ap	c 373	15	1.5	470	15	US-10-027-632-278381	Sequence 278381,
c 301	15	1.5	354	11	US-09-738-626-2743	Sequence 2743, Ap	c 374	15	1.5	470	15	US-10-027-632-278382	Sequence 278382,
c 302	15	1.5	361	12	US-09-918-995-7584	Sequence 7584, Ap	c 375	15	1.5	470	15	US-10-027-632-278383	Sequence 278383,
c 303	15	1.5	362	15	US-10-198-846-12626	Sequence 12626, A	c 376	15	1.5	472	11	US-09-998-598-678	Sequence 678, App
c 304	15	1.5	363	10	US-09-923-779-111	Sequence 111, App	c 377	15	1.5	472	12	US-09-918-995-22192	Sequence 22192, A
c 305	15	1.5	363	10	US-09-923-779-112	Sequence 112, App	c 378	15	1.5	475	11	US-09-764-847-413	Sequence 413, App
c 306	15	1.5	366	12	US-09-918-995-30171	Sequence 30171, A	c 379	15	1.5	475	15	US-10-092-154-413	Sequence 413, App
c 307	15	1.5	368	12	US-09-918-995-30102	Sequence 30102, A	c 380	15	1.5	476	12	US-09-918-995-14319	Sequence 14319, A
c 308	15	1.5	373	11	US-09-867-701-2195	Sequence 2195, Ap	c 381	15	1.5	480	11	US-09-924-035A-374	Sequence 374, App

C 382	15	1.5	481	10	US-09-864-761-14464	Sequence 14464, A	C 455	15	1.5	568	15	US-10-027-632-73890	Sequence 73890, A
C 383	15	1.5	481	15	US-10-027-632-78585	Sequence 78585, A	C 456	15	1.5	568	15	US-10-027-632-108903	Sequence 108903, A
C 384	15	1.5	481	15	US-10-027-632-78586	Sequence 78586, A	C 457	15	1.5	569	15	US-10-027-632-241522	Sequence 241522, A
C 385	15	1.5	481	15	US-10-027-632-78587	Sequence 78587, A	C 458	15	1.5	569	15	US-10-027-632-241523	Sequence 241523, A
C 386	15	1.5	481	15	US-10-027-632-78588	Sequence 78588, A	C 459	15	1.5	569	15	US-10-027-632-270154	Sequence 270154, A
C 387	15	1.5	481	15	US-10-027-632-195074	Sequence 195074, A	C 460	15	1.5	572	15	US-10-198-846-11211	Sequence 11211, A
C 388	15	1.5	481	15	US-10-027-632-195179	Sequence 195179, A	C 461	15	1.5	572	15	US-09-864-761-6605	Sequence 6605, Ap
C 389	15	1.5	481	15	US-10-198-846-5181	Sequence 5181, Ap	C 462	15	1.5	573	15	US-10-027-632-173367	Sequence 173367, A
C 390	15	1.5	486	10	US-09-215-450-2	Sequence 2, Appl	C 463	15	1.5	574	15	US-10-027-632-262947	Sequence 262947, A
C 391	15	1.5	486	15	US-10-027-632-82727	Sequence 82727, A	C 464	15	1.5	574	15	US-10-027-632-262948	Sequence 262948, A
C 392	15	1.5	486	15	US-10-027-632-302305	Sequence 302305, A	C 465	15	1.5	574	15	US-10-027-632-262949	Sequence 262949, A
C 393	15	1.5	492	15	US-10-198-846-2286	Sequence 2286, Ap	C 466	15	1.5	574	15	US-10-027-632-262950	Sequence 262950, A
C 394	15	1.5	493	10	US-09-604-287A-53	Sequence 53, Appl	C 467	15	1.5	574	15	US-10-027-632-262951	Sequence 262951, A
C 395	15	1.5	493	11	US-09-339-338-53	Sequence 53, Appl	C 468	15	1.5	574	15	US-10-027-632-278540	Sequence 278540, A
C 396	15	1.5	493	12	US-09-551-621-53	Sequence 53, Appl	C 469	15	1.5	575	15	US-10-027-632-303576	Sequence 303576, A
C 397	15	1.5	493	15	US-10-007-805-53	Sequence 53, Appl	C 470	15	1.5	576	15	US-10-027-632-246419	Sequence 246419, A
C 398	15	1.5	493	15	US-10-027-632-308704	Sequence 308704, A	C 471	15	1.5	576	15	US-10-027-632-246420	Sequence 246420, A
C 399	15	1.5	493	15	US-10-027-632-308705	Sequence 308705, A	C 472	15	1.5	576	15	US-10-027-632-246421	Sequence 246421, A
C 400	15	1.5	493	15	US-10-076-622-53	Sequence 53, Appl	C 473	15	1.5	577	15	US-10-027-632-37309	Sequence 37309, A
C 401	15	1.5	494	11	US-09-833-381-1944	Sequence 1944, Ap	C 474	15	1.5	579	15	US-10-027-632-224998	Sequence 224998, A
C 402	15	1.5	494	15	US-10-027-632-194597	Sequence 194597, A	C 475	15	1.5	579	15	US-10-038-010-19	Sequence 19, Appl
C 403	15	1.5	494	15	US-10-027-632-277532	Sequence 277532, A	C 476	15	1.5	580	10	US-09-864-761-9860	Sequence 9860, Ap
C 404	15	1.5	494	15	US-10-027-632-277533	Sequence 277533, A	C 477	15	1.5	580	15	US-10-027-632-40624	Sequence 40624, A
C 405	15	1.5	498	15	US-10-027-632-286705	Sequence 286705, A	C 478	15	1.5	581	15	US-10-027-632-229250	Sequence 229250, A
C 406	15	1.5	498	15	US-10-027-632-323086	Sequence 323086, A	C 479	15	1.5	581	15	US-10-027-632-258956	Sequence 258956, A
C 407	15	1.5	499	11	US-09-974-300-4768	Sequence 4768, Ap	C 480	15	1.5	585	11	US-09-738-632-2611	Sequence 2611, Ap
C 408	15	1.5	502	15	US-10-027-632-234123	Sequence 234123, A	C 481	15	1.5	585	15	US-10-027-632-187337	Sequence 187337, A
C 409	15	1.5	503	15	US-10-027-632-324037	Sequence 324037, A	C 482	15	1.5	585	15	US-10-027-632-187338	Sequence 187338, A
C 410	15	1.5	503	15	US-10-027-632-324038	Sequence 324038, A	C 483	15	1.5	585	15	US-10-027-632-223691	Sequence 223691, A
C 411	15	1.5	505	15	US-10-027-632-43441	Sequence 43441, A	C 484	15	1.5	586	15	US-10-027-632-209436	Sequence 209436, A
C 412	15	1.5	505	15	US-10-027-632-133808	Sequence 133808, A	C 485	15	1.5	589	15	US-10-062-254-193	Sequence 193, App
C 413	15	1.5	508	15	US-10-027-632-188232	Sequence 188232, A	C 486	15	1.5	589	15	US-10-027-632-269865	Sequence 269865, A
C 414	15	1.5	508	15	US-10-027-632-286282	Sequence 286282, A	C 487	15	1.5	590	15	US-10-027-632-230700	Sequence 230700, A
C 415	15	1.5	510	15	US-10-027-632-281761	Sequence 281761, A	C 488	15	1.5	591	15	US-10-027-632-213604	Sequence 213604, A
C 416	15	1.5	514	10	US-09-864-761-7848	Sequence 7848, Ap	C 489	15	1.5	591	15	US-10-027-632-213605	Sequence 213605, A
C 417	15	1.5	514	15	US-10-027-632-141263	Sequence 141263, A	C 490	15	1.5	591	15	US-10-027-632-213606	Sequence 213606, A
C 418	15	1.5	515	15	US-10-027-632-186407	Sequence 186407, A	C 491	15	1.5	592	15	US-10-027-632-131125	Sequence 131125, A
C 419	15	1.5	515	15	US-10-027-632-186408	Sequence 186408, A	C 492	15	1.5	594	10	US-09-864-761-6622	Sequence 6622, Ap
C 420	15	1.5	520	15	US-10-027-632-187838	Sequence 187838, A	C 493	15	1.5	596	15	US-10-027-632-90656	Sequence 90656, A
C 421	15	1.5	520	15	US-10-027-632-187839	Sequence 187839, A	C 494	15	1.5	596	15	US-10-027-632-90657	Sequence 90657, A
C 422	15	1.5	521	15	US-10-027-632-233717	Sequence 233717, A	C 495	15	1.5	596	15	US-10-027-632-247885	Sequence 247885, A
C 423	15	1.5	521	15	US-10-027-632-233717	Sequence 233717, A	C 496	15	1.5	598	15	US-10-027-632-190169	Sequence 190169, A
C 424	15	1.5	525	15	US-10-027-632-288815	Sequence 288815, A	C 497	15	1.5	598	15	US-10-027-632-233741	Sequence 233741, A
C 425	15	1.5	525	15	US-10-027-632-109621	Sequence 109621, A	C 498	15	1.5	599	15	US-10-027-632-5861	Sequence 5861, Ap
C 426	15	1.5	533	15	US-10-027-632-293138	Sequence 293138, A	C 499	15	1.5	599	15	US-10-027-632-5862	Sequence 5862, Ap
C 427	15	1.5	533	15	US-10-078-770-105	Sequence 105, App	C 500	15	1.5	599	15	US-10-027-632-5863	Sequence 5863, Ap
C 428	15	1.5	535	11	US-09-879-536-298	Sequence 298, App	C 501	15	1.5	603	15	US-10-027-632-88521	Sequence 88521, A
C 429	15	1.5	536	15	US-10-027-632-278539	Sequence 278539, A	C 502	15	1.5	603	15	US-10-027-632-303821	Sequence 303821, A
C 430	15	1.5	538	15	US-10-027-632-193906	Sequence 193906, A	C 503	15	1.5	604	15	US-10-027-632-17929	Sequence 17929, A
C 431	15	1.5	540	15	US-10-027-632-193907	Sequence 193907, A	C 504	15	1.5	604	15	US-10-027-632-136044	Sequence 136044, A
C 432	15	1.5	542	11	US-09-920-3008-1402	Sequence 5237, Ap	C 505	15	1.5	606	15	US-10-027-632-34757	Sequence 34757, A
C 433	15	1.5	542	15	US-10-033-528-1402	Sequence 1402, Ap	C 506	15	1.5	606	15	US-10-027-632-5882	Sequence 5882, Ap
C 434	15	1.5	543	15	US-10-027-632-116203	Sequence 116203, A	C 507	15	1.5	606	15	US-10-027-632-24689	Sequence 24689, A
C 435	15	1.5	543	15	US-10-027-632-89398	Sequence 89398, A	C 508	15	1.5	607	15	US-10-027-632-184953	Sequence 184953, A
C 436	15	1.5	543	15	US-10-027-632-303993	Sequence 303993, A	C 509	15	1.5	607	15	US-10-027-632-263628	Sequence 263628, A
C 437	15	1.5	545	15	US-10-027-632-57461	Sequence 57461, A	C 510	15	1.5	607	15	US-10-027-632-263629	Sequence 263629, A
C 438	15	1.5	546	15	US-10-027-632-70604	Sequence 70604, A	C 511	15	1.5	607	15	US-10-027-632-279422	Sequence 279422, A
C 439	15	1.5	546	15	US-10-027-632-179375	Sequence 179375, A	C 512	15	1.5	607	15	US-10-027-632-279423	Sequence 279423, A
C 440	15	1.5	546	15	US-10-027-632-200029	Sequence 200029, A	C 513	15	1.5	609	15	US-10-027-632-113221	Sequence 113221, A
C 441	15	1.5	546	15	US-10-171-581-131	Sequence 131, App	C 514	15	1.5	609	15	US-10-027-632-242009	Sequence 242009, A
C 442	15	1.5	548	10	US-09-864-761-11871	Sequence 11871, A	C 515	15	1.5	609	15	US-10-027-632-242010	Sequence 242010, A
C 443	15	1.5	548	15	US-10-027-632-140043	Sequence 140043, A	C 516	15	1.5	609	15	US-10-027-632-242011	Sequence 242011, A
C 444	15	1.5	551	15	US-10-027-632-91318	Sequence 91318, A	C 517	15	1.5	609	15	US-10-027-632-259426	Sequence 259426, A
C 445	15	1.5	551	15	US-10-027-632-278384	Sequence 278384, A	C 518	15	1.5	610	15	US-10-027-632-237688	Sequence 237688, A
C 446	15	1.5	551	15	US-10-027-632-278385	Sequence 278385, A	C 519	15	1.5	611	15	US-10-027-632-179281	Sequence 179281, A
C 447	15	1.5	551	15	US-10-027-632-278385	Sequence 278385, A	C 520	15	1.5	611	15	US-10-027-632-179282	Sequence 179282, A
C 448	15	1.5	556	11	US-09-796-692-8604	Sequence 8604, Ap	C 521	15	1.5	611	15	US-10-027-632-179283	Sequence 179283, A
C 449	15	1.5	556	15	US-10-040-862-8604	Sequence 8604, Ap	C 522	15	1.5	611	15	US-10-027-632-223058	Sequence 223058, A
C 450	15	1.5	559	15	US-10-027-632-180569	Sequence 180569, A	C 523	15	1.5	611	15	US-10-027-632-223059	Sequence 223059, A
C 451	15	1.5	559	15	US-10-027-632-223111	Sequence 223111, A	C 524	15	1.5	611	15	US-10-027-632-253522	Sequence 253522, A
C 452	15	1.5	559	15	US-10-027-632-247178	Sequence 247178, A	C 525	15	1.5	611	15	US-10-027-632-269792	Sequence 269792, A
C 453	15	1.5	567	15	US-10-027-632-84622	Sequence 84622, A	C 526	15	1.5	614	15	US-10-027-632-251058	Sequence 251058, A
C 454	15	1.5	567	15	US-10-027-632-272018	Sequence 272018, A	C 527	15	1.5	614	15	US-10-027-632-251059	Sequence 251059, A

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529	15	1.5	616	15	US-10-027-632-44973	Sequence 44973, A	602	15	1.5	675	15	US-10-027-632-213628	Sequence 213628,
530	15	1.5	616	15	US-10-027-632-131416	Sequence 131416,	603	15	1.5	676	15	US-10-027-632-218340	Sequence 218340,
531	15	1.5	616	15	US-10-027-632-131417	Sequence 131417,	c 604	15	1.5	676	15	US-10-027-632-247484	Sequence 247484,
532	15	1.5	616	15	US-10-027-632-131418	Sequence 131418,	605	15	1.5	679	15	US-10-027-632-139120	Sequence 139120,
533	15	1.5	616	15	US-10-027-632-131419	Sequence 131419,	606	15	1.5	681	11	US-09-989-920-53	Sequence 53, Appl
534	15	1.5	616	15	US-10-027-632-217396	Sequence 217396,	607	15	1.5	681	15	US-10-027-632-184945	Sequence 184945,
535	15	1.5	616	15	US-10-027-632-217397	Sequence 217397,	608	15	1.5	682	15	US-10-027-632-229908	Sequence 229908,
536	15	1.5	616	15	US-10-027-632-217398	Sequence 217398,	609	15	1.5	682	15	US-10-027-632-229909	Sequence 229909,
537	15	1.5	617	15	US-10-027-632-250750	Sequence 250750,	610	15	1.5	684	15	US-10-027-632-14605	Sequence 14605, A
538	15	1.5	617	15	US-10-027-632-250751	Sequence 250751,	c 611	15	1.5	684	15	US-10-027-632-14606	Sequence 14606, A
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547	15	1.5	622	15	US-10-027-632-300435	Sequence 300435,	c 620	15	1.5	706	15	US-10-027-632-116529	Sequence 116529,
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552	15	1.5	625	15	US-10-027-632-68517	Sequence 68517, A	c 626	15	1.5	715	15	US-10-027-632-26405	Sequence 26405, A
553	15	1.5	625	15	US-10-027-632-192335	Sequence 192335,	c 627	15	1.5	720	10	US-09-910-943-105	Sequence 105, App
554	15	1.5	625	15	US-10-027-632-192336	Sequence 192336,	c 628	15	1.5	725	15	US-10-027-632-157268	Sequence 157268,
555	15	1.5	625	15	US-10-027-632-192337	Sequence 192337,	c 629	15	1.5	725	15	US-10-027-632-163230	Sequence 163230,
556	15	1.5	627	15	US-10-027-632-6039	Sequence 6039, Ap	c 630	15	1.5	729	10	US-09-910-943-104	Sequence 104, App
557	15	1.5	627	15	US-10-027-632-64174	Sequence 64174, A	c 631	15	1.5	729	15	US-10-027-632-128732	Sequence 128732,
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559	15	1.5	627	15	US-10-027-632-107874	Sequence 107874,	c 633	15	1.5	732	15	US-10-027-632-128731	Sequence 128731,
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562	15	1.5	630	15	US-10-027-632-232219	Sequence 232219,	c 636	15	1.5	745	15	US-10-027-632-21881	Sequence 21881, A
563	15	1.5	631	15	US-10-027-632-46216	Sequence 46216, A	c 637	15	1.5	748	10	US-09-910-943-172	Sequence 172, App
564	15	1.5	631	15	US-10-027-632-46216	Sequence 46216, A	c 638	15	1.5	749	15	US-10-027-632-137322	Sequence 137322,
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566	15	1.5	631	15	US-10-027-632-309007	Sequence 309007,	c 640	15	1.5	757	15	US-10-027-632-153307	Sequence 153307,
567	15	1.5	633	15	US-10-027-632-113626	Sequence 113626,	c 641	15	1.5	757	15	US-10-027-632-153308	Sequence 153308,
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569	15	1.5	635	15	US-10-027-632-281946	Sequence 281946,	c 643	15	1.5	761	15	US-10-062-254-195	Sequence 195, App
570	15	1.5	635	15	US-10-198-846-8146	Sequence 8146, Ap	c 644	15	1.5	762	11	US-09-995-598-39	Sequence 39, Appl
571	15	1.5	636	11	US-09-738-626-2734	Sequence 2734, Ap	c 645	15	1.5	766	10	US-09-864-761-17873	Sequence 17873, A
572	15	1.5	637	15	US-10-027-632-225670	Sequence 225670,	c 646	15	1.5	770	11	US-09-974-300-2057	Sequence 2057, Ap
573	15	1.5	637	15	US-10-027-632-293496	Sequence 293496,	c 647	15	1.5	778	15	US-10-144-929-58	Sequence 58, Appl
574	15	1.5	638	15	US-10-027-632-114302	Sequence 114302,	c 648	15	1.5	781	15	US-10-027-632-987	Sequence 987, App
575	15	1.5	638	15	US-10-027-632-137669	Sequence 137669,	c 649	15	1.5	789	11	US-09-903-410-25	Sequence 25, Appl
576	15	1.5	641	15	US-10-027-632-46858	Sequence 46858, A	c 650	15	1.5	789	15	US-10-027-805-25	Sequence 25, Appl
577	15	1.5	644	15	US-10-027-632-104913	Sequence 104913,	c 651	15	1.5	795	10	US-10-027-804-25	Sequence 25, Appl
578	15	1.5	644	15	US-10-027-632-133338	Sequence 133338,	c 652	15	1.5	795	10	US-09-815-242-7524	Sequence 7524, Ap
579	15	1.5	647	15	US-10-027-632-80247	Sequence 80247, A	c 653	15	1.5	801	15	US-10-027-632-153514	Sequence 153514,
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581	15	1.5	648	10	US-09-867-550-765	Sequence 765, App	c 655	15	1.5	810	11	US-09-966-881-23	Sequence 23, Appl
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583	15	1.5	650	15	US-10-027-632-218599	Sequence 218599,	c 657	15	1.5	815	15	US-10-027-632-168064	Sequence 168064,
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585	15	1.5	650	15	US-10-027-632-300691	Sequence 300691,	c 659	15	1.5	817	15	US-10-027-632-31248	Sequence 31248, A
586	15	1.5	652	11	US-09-864-864-156	Sequence 156, App	c 660	15	1.5	822	15	US-10-027-632-807	Sequence 807, App
587	15	1.5	653	15	US-10-027-632-79820	Sequence 79820, A	c 661	15	1.5	822	15	US-10-027-632-170606	Sequence 170606,
588	15	1.5	653	15	US-10-027-632-80742	Sequence 80742, A	c 662	15	1.5	824	15	US-10-027-632-167201	Sequence 167201,
589	15	1.5	653	15	US-10-027-632-80871	Sequence 80871, A	c 663	15	1.5	824	15	US-10-027-632-167202	Sequence 167202,
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591	15	1.5	655	15	US-10-027-632-227367	Sequence 227367,	c 665	15	1.5	826	15	US-10-027-632-127913	Sequence 127913,
592	15	1.5	662	15	US-10-027-632-277062	Sequence 277062,	c 666	15	1.5	830	15	US-10-027-632-171403	Sequence 171403,
593	15	1.5	663	12	US-09-899-493-46	Sequence 46, Appl	c 667	15	1.5	830	15	US-10-027-632-171403	Sequence 171403,
594	15	1.5	663	15	US-10-027-632-250796	Sequence 250796,	c 668	15	1.5	833	15	US-10-198-846-9335	Sequence 9335, Ap
595	15	1.5	663	15	US-10-027-632-250797	Sequence 250797,	c 669	15	1.5	833	15	US-10-027-632-165942	Sequence 165942,
596	15	1.5	665	15	US-10-027-632-250797	Sequence 250797,	c 670	15	1.5	836	15	US-10-027-632-165943	Sequence 165943,
597	15	1.5	666	15	US-10-027-632-276047	Sequence 276047,	c 671	15	1.5	836	15	US-10-027-632-165944	Sequence 165944,
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					US-10-027-632-101602	Sequence 101602,	c 675	15	1.5	840	15	US-10-027-632-166145	Sequence 166145,

c 674	1.5	842	15	US-10-027-632-146868	Sequence 146868,	c 747	1.5	1375	15	US-10-091-572-907	Sequence 907, App
c 675	1.5	843	15	US-10-027-632-159952	Sequence 159952,	c 748	1.5	1375	15	US-10-091-572-908	Sequence 908, App
c 676	1.5	851	15	US-10-027-632-8924	Sequence 8924, Ap	c 749	1.5	1383	15	US-10-033-078-3	Sequence 3, Appli
c 677	1.5	855	15	US-10-027-632-9798	Sequence 9798, Ap	c 750	1.5	1393	11	US-09-974-300-1687	Sequence 1687, Ap
c 678	1.5	855	15	US-10-027-632-163615	Sequence 163615,	c 751	1.5	1399	11	US-09-974-300-1163	Sequence 1163, Ap
c 679	1.5	861	15	US-10-027-632-173997	Sequence 173997,	c 752	1.5	1407	11	US-09-974-300-2053	Sequence 2053, Ap
c 680	1.5	861	15	US-10-027-632-173998	Sequence 173998,	c 753	1.5	1446	11	US-09-938-842A-802	Sequence 802, App
c 681	1.5	871	15	US-10-027-632-171373	Sequence 171373,	c 754	1.5	1476	15	US-10-322-149-13	Sequence 13, Appl
c 682	1.5	871	15	US-10-027-632-171374	Sequence 171374,	c 755	1.5	1492	15	US-10-078-770-113	Sequence 113, App
c 683	1.5	900	11	US-09-738-626-643	Sequence 643, App	c 756	1.5	1507	8	US-08-781-986A-361	Sequence 361, App
c 684	1.5	907	15	US-10-004-717-65	Sequence 65, Appl	c 757	1.5	1542	11	US-09-860-670-66	Sequence 66, Appl
c 685	1.5	908	15	US-10-027-632-159048	Sequence 159048,	c 758	1.5	1549	11	US-10-001-835-102	Sequence 102, App
c 686	1.5	915	15	US-10-144-929-54	Sequence 54, Appl	c 759	1.5	1559	11	US-09-938-842A-1762	Sequence 1762, Ap
c 687	1.5	917	15	US-10-198-846-11251	Sequence 11251, A	c 760	1.5	1603	15	US-10-027-632-260006	Sequence 260006,
c 688	1.5	920	15	US-10-198-846-3396	Sequence 3396, Ap	c 761	1.5	1605	12	US-09-986-480-21	Sequence 21, Appl
c 689	1.5	928	15	US-10-027-632-33634	Sequence 33634, A	c 762	1.5	1605	12	US-09-895-298-42	Sequence 42, Appl
c 690	1.5	942	11	US-09-738-626-3210	Sequence 3210, Ap	c 763	1.5	1606	15	US-10-098-841-323	Sequence 323, App
c 691	1.5	944	15	US-10-027-632-159953	Sequence 159953,	c 764	1.5	1614	11	US-09-917-800A-1525	Sequence 1525, Ap
c 692	1.5	982	15	US-10-027-632-265049	Sequence 265049,	c 765	1.5	1629	15	US-10-027-632-262689	Sequence 262689,
c 693	1.5	992	11	US-09-974-300-1716	Sequence 1716, Ap	c 766	1.5	1744	11	US-09-833-381-1943	Sequence 1943, Ap
c 694	1.5	996	10	US-09-900-715-1	Sequence 1, Appli	c 767	1.5	1750	10	US-09-925-301-403	Sequence 403, App
c 695	1.5	998	15	US-10-106-698-1599	Sequence 1599, Ap	c 768	1.5	1797	10	US-09-875-811-11	Sequence 11, Appl
c 696	1.5	1011	11	US-09-938-842A-1719	Sequence 1719, Ap	c 769	1.5	1818	10	US-09-875-811-7	Sequence 7, Appli
c 697	1.5	1021	11	US-09-954-456-186	Sequence 186, App	c 770	1.5	1823	15	US-10-171-581-126	Sequence 126, App
c 698	1.5	1021	11	US-09-954-456-941	Sequence 941, App	c 771	1.5	1824	15	US-10-044-090-372	Sequence 372, App
c 699	1.5	1050	10	US-09-886-468-4	Sequence 4, Appli	c 772	1.5	1840	11	US-09-895-913A-139	Sequence 139, App
c 700	1.5	1078	10	US-09-923-779-147	Sequence 147, App	c 773	1.5	1849	15	US-10-027-632-33099	Sequence 33099, A
c 701	1.5	1078	11	US-09-835-948-28	Sequence 28, Appl	c 774	1.5	1849	15	US-10-027-632-39100	Sequence 39100, A
c 702	1.5	1078	11	US-09-835-948-29	Sequence 29, Appl	c 775	1.5	1849	15	US-10-027-632-39101	Sequence 39101, A
c 703	1.5	1078	15	US-10-097-340-190	Sequence 190, App	c 776	1.5	1849	15	US-10-027-632-39102	Sequence 39102, A
c 704	1.5	1078	15	US-10-171-311-140	Sequence 140, App	c 777	1.5	1859	11	US-09-915-582-23	Sequence 23, Appli
c 705	1.5	1078	15	US-10-205-823-267	Sequence 267, App	c 778	1.5	1866	10	US-09-875-811-3	Sequence 3, Appli
c 706	1.5	1078	15	US-10-177-293-299	Sequence 299, App	c 779	1.5	1868	11	US-09-938-842A-5068	Sequence 5068, Ap
c 707	1.5	1094	11	US-09-070-927A-640	Sequence 640, App	c 780	1.5	1936	11	US-09-822-830A-291	Sequence 291, App
c 708	1.5	1096	11	US-09-974-300-2393	Sequence 2393, Ap	c 781	1.5	1937	11	US-09-822-830A-364	Sequence 364, App
c 709	1.5	1107	15	US-10-156-761-3873	Sequence 3873, Ap	c 782	1.5	1946	15	US-10-006-852-9	Sequence 9, Appli
c 710	1.5	1110	15	US-10-027-632-118261	Sequence 118261,	c 783	1.5	1967	15	US-10-027-632-264119	Sequence 264119,
c 711	1.5	1113	11	US-09-993-844-9	Sequence 9, Appli	c 784	1.5	1970	12	US-09-952-680A-11	Sequence 11, Appl
c 712	1.5	1125	11	US-09-798-584-2	Sequence 2, Appli	c 785	1.5	1971	10	US-09-875-811-9	Sequence 9, Appli
c 713	1.5	1127	15	US-10-171-311-138	Sequence 138, App	c 786	1.5	1971	10	US-09-942-446-3	Sequence 3, Appli
c 714	1.5	1127	15	US-10-205-823-265	Sequence 265, App	c 787	1.5	1973	15	US-10-027-632-98458	Sequence 98458, A
c 715	1.5	1127	15	US-10-102-524-1705	Sequence 1705, Ap	c 788	1.5	1973	15	US-10-027-632-98459	Sequence 98459, A
c 716	1.5	1137	11	US-09-974-300-2309	Sequence 2309, Ap	c 789	1.5	1973	15	US-10-027-632-98460	Sequence 98460, A
c 717	1.5	1144	11	US-09-974-300-804	Sequence 804, App	c 790	1.5	1977	11	US-09-938-842A-1120	Sequence 1120, Ap
c 718	1.5	1167	11	US-09-738-626-3042	Sequence 3042, Ap	c 791	1.5	1982	15	US-10-027-632-97898	Sequence 97898, A
c 719	1.5	1173	15	US-10-027-632-116754	Sequence 116754,	c 792	1.5	1982	15	US-10-027-632-97899	Sequence 97899, A
c 720	1.5	1173	15	US-10-106-698-2123	Sequence 2123, Ap	c 793	1.5	1992	10	US-09-875-811-5	Sequence 5, Appli
c 721	1.5	1174	11	US-09-938-842A-3677	Sequence 3677, Ap	c 794	1.5	1992	15	US-10-027-632-263202	Sequence 263202,
c 722	1.5	1176	15	US-10-027-632-119084	Sequence 119084,	c 795	1.5	1992	15	US-10-027-632-263203	Sequence 263203,
c 723	1.5	1186	15	US-10-027-632-123952	Sequence 123952,	c 796	1.5	1992	15	US-10-027-632-263204	Sequence 263204,
c 724	1.5	1224	15	US-10-027-632-123952	Sequence 123952,	c 797	1.5	2000	11	US-09-938-842A-3396	Sequence 3396, Ap
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ALIGNMENTS

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; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
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US-09-918-995-24455

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RESULT 2
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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
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RESULT 3
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; Sequence 124906, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124906
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-124906

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Query Match	2.0%;	Score 19;	DB 12;	Length 502;
Best Local Similarity	100.0%;	Pred. NO. 6.5;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	900	TCGAGAGGGAATAGAATTG	918	
Db	174	TGAGAGGGAATAGAATTG	192	

RESULT 4
US-10-274-266-1
; Sequence 1, Application US/10274266
; Publication No. US20030059893A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins, Nucleic Acid Molecules Encoding
; FILE REFERENCE: CLO00839DIV
; CURRENT APPLICATION NUMBER: US/10/274,266
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-274-266-1

Query Match 2.0%; Score 19; DB 15; Length 1146;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 TCTGGATACTGCTCGTTT 489
|||
Db 639 TCTGGATACTGCTCGTTT 657

RESULT 5
US-09-731-872-15
; Sequence 15, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 15
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 101..517
; NAME/KEY: sig_peptide
; LOCATION: 101..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.57613483592743
; OTHER INFORMATION: seq FLCGLMALCPRQA/TR
US-09-731-872-15

Query Match 2.0%; Score 19; DB 11; Length 1755;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 TCTGGATACTGCTCGTTT 489
|||
Db 737 TCTGGATACTGCTCGTTT 755

RESULT 6
US-09-731-872-14

; Sequence 14, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 101..1243
; NAME/KEY: sig_peptide
; LOCATION: 101..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.57142340200611
; OTHER INFORMATION: seq FLCGLMALCPRQA/TR
US-09-731-872-14

Query Match 2.0%; Score 19; DB 11; Length 1759;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 TCTGGATACTGCTCGTTT 489
|||
Db 739 TCTGGATACTGCTCGTTT 757

RESULT 7
US-10-128-714-87/c
; Sequence 87, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Weng
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-87

Query Match 2.0%; Score 19; DB 15; Length 2352;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 156 CAAAGCAGAGGTTGAAAGC 174
Db 2018 CAAAGCAGAGGTTGAAAGC 2000

RESULT 8
US-10-128-714-5087/c
; Sequence 5087, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5087
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-5087

Query Match 2.0%; Score 19; DB 15; Length 2352;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 156 CAAAGCAGAGGTTGAAAGC 174
Db 2018 CAAAGCAGAGGTTGAAAGC 2000

RESULT 9
US-10-274-266-3
; Sequence 3, Application US/10274266
; Publication No. US20030059893A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins, Nucleic Acid Molecules Encoding
; TITLE OF INVENTION: Secreted Proteins, And Uses Thereof
; FILE REFERENCE: CL0008391V
; CURRENT APPLICATION NUMBER: US/10/274,266
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3144
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-274-266-3

Query Match 2.0%; Score 19; DB 15; Length 3144;
Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 TCTGGATACCTGCTCGTTTT 489
Db 1638 TCTGGATACCTGCTCGTTTT 1656

RESULT 10
US-09-918-995-11651
; Sequence 11651, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11651
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-11651

Query Match 1.9%; Score 18; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 625 GAAAAGCCACACACATA 642
Db 464 GAAAAGCCACACACATA 481

RESULT 11
US-10-027-632-233560
; Sequence 233560, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233560
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-233560

Query Match 1.9%; Score 18; DB 15; Length 559;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 TGATTATTTGGGTTCA 827
 Db 491 TGATTATTTGGGTTCA 508

RESULT 12
 US-09-974-300-6602/c
 ; Sequence 6602, Application US/09974300
 ; Patent No. US20020146721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Clausen, Ib Groth
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; FILE REFERENCE: Expression
 ; CURRENT APPLICATION NUMBER: US/09/974,300
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 09/680,598
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/279,526
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 8481
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6602
 ; LENGTH: 828
 ; TYPE: DNA
 ; ORGANISM: Bacillus clausii
 US-09-974-300-6602

Query Match 1.9%; Score 18; DB 11; Length 828;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 346 AATGTTGCCAAATATGCT 363
 Db 291 AATGTTGCCAAATATGCT 274

RESULT 13
 US-09-938-842A-4346
 ; Sequence 4346, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 4346
 ; LENGTH: 996
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-4346

Query Match 1.9%; Score 18; DB 11; Length 996;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 912 AGAATTGATGGAATAATC 929
 Db 258 AGAATTGATGGAATAATC 275

RESULT 14
 US-09-938-842A-5127/c
 ; Sequence 5127, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 5127
 ; LENGTH: 996
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-5127

Query Match 1.9%; Score 18; DB 11; Length 996;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 912 AGAATTGATGGAATAATC 929
 Db 739 AGAATTGATGGAATAATC 722

RESULT 15
 US-10-027-632-259728
 ; Sequence 259728, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 259728
 ; LENGTH: 2338
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-259728

Query Match 1.9%; Score 18; DB 15; Length 2338;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 AAAGCCAACCATATTT 645
| | | | | | | | | | | | | | | | | |
Db 1734 AAAGCCAACCATATTT 1751

Search completed: July 31, 2003, 13:50:22
Job time : 313 secs

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 11:01:27 ; Search time 1720 Seconds
(without alignments)
9152.333 Million cell updates/sec

Title: US-09-992-430B-21
Perfect score: 972
Sequence: 1 atgttcaagatacaaaagt.....ttgagcatctggagatcaat 972

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: em_estba:*

2: em_estbha:*

3: em_estin:*

4: em_estm:*

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6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	2.2	520	10	AW239816
2	20	2.1	202	12	BE859322
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4	20	2.1	580	17	BH54885
5	20	2.1	583	9	AA453969
6	20	2.1	592	17	PT005G13U

1	21	2.2	520	10	AW239816
2	20	2.1	202	12	BE859322
3	20	2.1	578	9	AA460603
4	20	2.1	580	17	BH54885
5	20	2.1	583	9	AA453969
6	20	2.1	592	17	PT005G13U

80	19	2.0	699	12	BE908297	601500589	153	18	1.9	495	9	AU242478	AU242478
81	19	2.0	725	12	EG028730	602229216	C 154	18	1.9	496	9	AI958031	AI958031
82	19	2.0	741	17	BH470939	BH470939	155	18	1.9	500	9	AU088428	AU088428
83	19	2.0	743	9	AJ450618	AJ450618	156	18	1.9	503	9	AL365864	AL365864
84	19	2.0	743	14	BQ424840	BQ424840	C 157	18	1.9	503	17	BH352659	BH352659
85	19	2.0	745	13	BG154248	BG154248	C 158	18	1.9	506	9	AI140336	AI140336
86	19	2.0	745	14	BQ435491	BQ435491	C 159	18	1.9	506	9	AI140336	AI140336
87	19	2.0	755	14	BQ435491	BQ435491	C 160	18	1.9	507	14	BM883476	BM883476
88	19	2.0	762	14	BM803372	BM803372	C 161	18	1.9	510	12	EG516069	EG516069
89	19	2.0	771	9	AZ193368	AZ193368	C 162	18	1.9	511	13	BI745273	BI745273
90	19	2.0	779	9	AI420467	AI420467	C 163	18	1.9	513	10	AM150267	AM150267
91	19	2.0	793	13	BJ130459	BJ130459	C 164	18	1.9	515	14	BQ490600	BQ490600
92	19	2.0	800	10	BE311605	BE311605	C 165	18	1.9	516	14	BM883508	BM883508
93	19	2.0	807	9	AI121147	AI121147	C 166	18	1.9	518	10	AV965836	AV965836
94	19	2.0	825	13	BI857657	BI857657	C 167	18	1.9	522	13	BM338184	BM338184
95	19	2.0	836	9	AF034561	AF034561	C 168	18	1.9	538	17	TM35810P	TM35810P
96	19	2.0	852	17	AZ192066	AZ192066	C 169	18	1.9	540	17	AQ504874	AQ504874
97	19	2.0	853	13	BI333253	BI333253	C 170	18	1.9	552	17	AZ908153	AZ908153
98	19	2.0	858	17	BH720064	BH720064	C 171	18	1.9	554	17	AQ500945	AQ500945
99	19	2.0	859	12	BF577140	BF577140	C 172	18	1.9	560	13	BM190310	BM190310
100	19	2.0	864	12	BF695941	BF695941	C 173	18	1.9	562	9	AA037768	AA037768
101	19	2.0	888	14	BQ217137	BQ217137	C 174	18	1.9	581	13	BI814536	BI814536
102	19	2.0	899	14	BQ876592	BQ876592	C 175	18	1.9	591	17	BH103018	BH103018
103	19	2.0	925	13	BI912675	BI912675	C 176	18	1.9	601	9	AA660498	AA660498
104	19	2.0	937	14	BQ929045	BQ929045	C 177	18	1.9	607	13	BJ275391	BJ275391
105	19	2.0	950	12	EG289481	EG289481	C 178	18	1.9	608	14	BQ596074	BQ596074
106	19	2.0	1003	14	BQ082301	BQ082301	C 179	18	1.9	612	17	AZ413764	AZ413764
107	19	2.0	1010	17	CNS05FK1	CNS05FK1	C 180	18	1.9	620	14	W58369	W58369
108	19	2.0	1047	13	BM478115	BM478115	C 181	18	1.9	625	17	TA1E10Q	TA1E10Q
109	19	2.0	1069	13	BM557491	BM557491	C 182	18	1.9	625	17	AQ653087	AQ653087
110	19	2.0	1119	13	BM543065	BM543065	C 183	18	1.9	629	17	AG153190	AG153190
111	19	2.0	1138	17	BI11122	BI11122	C 184	18	1.9	636	17	AZ383689	AZ383689
112	18	1.9	155	17	BH820991	BH820991	C 185	18	1.9	640	10	BB610625	BB610625
113	18	1.9	161	17	BH83481	BH83481	C 186	18	1.9	641	17	AQ324799	AQ324799
114	18	1.9	211	9	AV162076	AV162076	C 187	18	1.9	644	12	BF648209	BF648209
115	18	1.9	217	10	AQ249058	AQ249058	C 188	18	1.9	646	9	AU237048	AU237048
116	18	1.9	227	10	BB074489	BB074489	C 189	18	1.9	646	14	BQ553851	BQ553851
117	18	1.9	228	17	BH832567	BH832567	C 190	18	1.9	652	13	BJ348361	BJ348361
118	18	1.9	260	17	CNS00VXC	CNS00VXC	C 191	18	1.9	659	17	AG015527	AG015527
119	18	1.9	291	17	BH789421	BH789421	C 192	18	1.9	679	17	AG044939	AG044939
120	18	1.9	308	10	AV300623	AV300623	C 193	18	1.9	689	17	AQ956644	AQ956644
121	18	1.9	312	14	Z33949	Z33949	C 194	18	1.9	690	17	AZ383805	AZ383805
122	18	1.9	314	10	BB548876	BB548876	C 195	18	1.9	701	14	BQ655135	BQ655135
123	18	1.9	315	10	BB255599	BB255599	C 196	18	1.9	707	17	AZ976860	AZ976860
124	18	1.9	319	10	AW480082	AW480082	C 197	18	1.9	718	17	AQ854086	AQ854086
125	18	1.9	333	12	BF590415	BF590415	C 198	18	1.9	724	17	AQ329870	AQ329870
126	18	1.9	335	17	BH752588	BH752588	C 199	18	1.9	731	10	AV384022	AV384022
127	18	1.9	342	10	BB560598	BB560598	C 200	18	1.9	742	17	AZ993687	AZ993687
128	18	1.9	359	10	AW435544	AW435544	C 201	18	1.9	746	17	AZ973355	AZ973355
129	18	1.9	387	17	AQ205678	AQ205678	C 202	18	1.9	752	17	BQ0686	BQ0686
130	18	1.9	393	12	EG561482	EG561482	C 203	18	1.9	773	17	AQ468888	AQ468888
131	18	1.9	400	14	BQ293743	BQ293743	C 204	18	1.9	777	17	BH770459	BH770459
132	18	1.9	403	10	AW827576	AW827576	C 205	18	1.9	783	14	BQ137631	BQ137631
133	18	1.9	433	10	AV855203	AV855203	C 206	18	1.9	786	9	AL566376	AL566376
134	18	1.9	436	13	BI202051	BI202051	C 207	18	1.9	793	17	BH728594	BH728594
135	18	1.9	436	13	BI208842	BI208842	C 208	18	1.9	803	17	BM604923	BM604923
136	18	1.9	436	14	BQ484483	BQ484483	C 209	18	1.9	816	9	AA979820	AA979820
137	18	1.9	443	9	AI757170	AI757170	C 210	18	1.9	823	12	BF168427	BF168427
138	18	1.9	443	17	AQ149892	AQ149892	C 211	18	1.9	835	9	AJ452569	AJ452569
139	18	1.9	447	17	BH2423	BH2423	C 212	18	1.9	837	17	AZ534802	AZ534802
140	18	1.9	454	9	AI163359	AI163359	C 213	18	1.9	842	12	EG739872	EG739872
141	18	1.9	456	12	BG561895	BG561895	C 214	18	1.9	844	17	AZ681624	AZ681624
142	18	1.9	456	17	AQ894054	AQ894054	C 215	18	1.9	844	17	AZ681624	AZ681624
143	18	1.9	461	14	BQ244475	BQ244475	C 216	18	1.9	850	17	BH541920	BH541920
144	18	1.9	465	13	BI859457	BI859457	C 217	18	1.9	863	17	CNS00ABR	CNS00ABR
145	18	1.9	466	9	AL693585	AL693585	C 218	18	1.9	868	17	AZ667930	AZ667930
146	18	1.9	467	17	AQ624333	AQ624333	C 219	18	1.9	898	17	AZ530682	AZ530682
147	18	1.9	473	12	BG725117	BG725117	C 220	18	1.9	907	17	AZ670338	AZ670338
148	18	1.9	474	12	EG561481	EG561481	C 221	18	1.9	931	14	BQ895624	BQ895624
149	18	1.9	476	17	AQ462860	AQ462860	C 222	18	1.9	968	12	BG208890	BG208890
150	18	1.9	482	12	BG517042	BG517042	C 223	18	1.9				
151	18	1.9	485	12	BF043063	BF043063	C 224	18	1.9				
152	18	1.9	494	17	AQ078844	AQ078844	C 225	18	1.9				

c 226	18	1.9	968	12	BG462141	BG462141 RST45155	299	17	1.7	367	17	BH881796	BH881796 hv28b03.g
c 227	18	1.9	972	17	CNS02EFO	AL193677 TETraodon	c 300	17	1.7	368	9	AI470248	AI470248 t1j7G05.x
c 228	18	1.9	986	14	BQ227634	BQ227634 AGENCOURT	c 301	17	1.7	369	13	BQ38491	BQ38491 R7038491
c 229	18	1.9	989	12	BG869189	BG869189 602789072	c 302	17	1.7	370	17	AQ280064	AQ280064 CITBI-EI-
c 230	18	1.9	1009	13	B1830589	B1830589 603073120	c 303	17	1.7	372	9	AA818228	AA818228 UI-R-A0-a
c 231	18	1.9	1038	12	BF678823	BF678823 602513126	c 304	17	1.7	372	9	AA186746	AA186746 AV186746
c 232	18	1.9	1068	12	BF531186	BF531186 602091174	c 305	17	1.7	373	9	AA252795	AA252795 z627a12.b
c 233	18	1.9	1114	12	BG547370	BG547370 602574778	c 306	17	1.7	373	17	AQ563048	AQ563048 HS 5301.A
c 234	18	1.9	1376	12	BE744646	BE744646 601577484	c 307	17	1.7	374	17	A2430751	A2430751 IM0215D20
c 235	18	1.9	1522	11	AK005882	AK005882 Mus muscu	c 308	17	1.7	375	9	AI029427	AI029427 UI-R-C0-i
c 236	17	1.7	138	17	AQ079932	AQ079932 CIT-HSP-2	c 309	17	1.7	375	14	C42506	C42506 C42506 Yuji
c 237	17	1.7	144	12	BE764667	BE764667 FM2-NT007	c 310	17	1.7	382	9	AA046522	AA046522 zk62f04.b
c 238	17	1.7	178	12	BF771253	BF771253 RC2-IT004	c 311	17	1.7	385	14	T97417	T97417 yes3h01.r1
c 239	17	1.7	178	12	BF920486	BF920486 QV0-NT010	c 312	17	1.7	386	10	AW357152	AW357152 40021 MAR
c 240	17	1.7	193	9	AA060952	AA060952 m380h12.r	c 313	17	1.7	388	13	B1121099	B1121099 F028P60Y
c 241	17	1.7	193	10	BB213891	BB213891 BB213891	c 314	17	1.7	391	10	AW360330	AW360330 47894 MAR
c 242	17	1.7	193	14	H34245	H34245 EST110974.R	c 315	17	1.7	392	17	AQ003737	AQ003737 CpG0363A
c 243	17	1.7	196	12	BG29287	BG29287 CC-esf1CL	c 316	17	1.7	395	17	AZ715020	AZ715020 RPCI-24-1
c 244	17	1.7	198	13	B1643414	B1643414 RSI_B08.S	c 317	17	1.7	397	9	AA991355	AA991355 o8s1e12.8
c 245	17	1.7	224	10	BE051426	BE051426 za82f12.g	c 318	17	1.7	397	13	BQ7070348	BQ7070348 BJ070348
c 246	17	1.7	229	12	BG139606	BG139606 EST479964	c 319	17	1.7	398	17	AQ845497	AQ845497 LMAJFV1.1
c 247	17	1.7	235	10	BB065417	BB065417 BB065417	c 320	17	1.7	398	17	AQ127189	AQ127189 HS 3042.B
c 248	17	1.7	236	10	BB582827	BB582827 BB582827	c 321	17	1.7	400	17	BH881795	BH881795 hv28b03.b
c 249	17	1.7	237	10	BE142063	BE142063 CM3-HT013	c 322	17	1.7	402	12	BF892586	BF892586 QV1-MP013
c 250	17	1.7	254	12	BF920487	BF920487 QV0-NT010	c 323	17	1.7	402	17	B74335	B74335 CIT-HSP-204
c 251	17	1.7	256	10	AV440385	AV440385 AV440385	c 324	17	1.7	404	13	B1325478	B1325478 949039F10
c 252	17	1.7	263	17	AZ328389	AZ328389 IM0052F12	c 325	17	1.7	405	12	BE863227	BE863227 UI-M-BH0-
c 253	17	1.7	264	13	B1626279	B1626279 RH66849.5	c 326	17	1.7	406	17	AQ544703	AQ544703 CITBI-EI-
c 254	17	1.7	267	17	AQ350411	AQ350411 RHC111-12	c 327	17	1.7	413	13	B1130057	B1130057 G101877Y
c 255	17	1.7	274	12	BG139601	BG139601 EST479959	c 328	17	1.7	415	17	AF192545	AF192545 AF192545
c 256	17	1.7	282	10	BB046375	BB046375 QV0-NT010	c 329	17	1.7	416	10	AW379808	AW379808 RC3-HT025
c 257	17	1.7	282	10	BB046375	BB046375 BB046375	c 330	17	1.7	416	12	BF198160	BF198160 247009 NA
c 258	17	1.7	286	12	BG520462	BG520462 p816h07.Y	c 331	17	1.7	417	17	BH876508	BH876508 hr31e06.g
c 259	17	1.7	289	9	AV259207	AV259207 AV259207	c 332	17	1.7	418	9	AI299131	AI299131 qtl4h10.x
c 260	17	1.7	290	14	BQ164880	BQ164880 EST610749	c 333	17	1.7	419	17	AQ338183	AQ338183 HS 2215.B
c 261	17	1.7	291	9	AV114792	AV114792 AV114792	c 334	17	1.7	420	10	BE192157	BE192157 db8b10.x
c 262	17	1.7	291	17	AQ116868	AQ116868 HS 2255.A	c 335	17	1.7	421	10	AW871992	AW871992 da95G02.Y
c 263	17	1.7	292	10	BB359000	BB359000 BB359000	c 336	17	1.7	421	14	BQ637637	BQ637637 he12f09.Y
c 264	17	1.7	307	14	BQ168387	BQ168387 WHE2102.D	c 337	17	1.7	425	12	BG629736	BG629736 CC-esf1CL
c 265	17	1.7	308	10	AM086543	AM086543 ga01g05.x	c 338	17	1.7	425	14	BQ129202	BQ129202 i3j34f08.x
c 266	17	1.7	308	13	BM153847	BM153847 168 Giant	c 339	17	1.7	426	9	AI179145	AI179145 EST222829
c 267	17	1.7	311	10	AM098821	AM098821 ga01g05.Y	c 340	17	1.7	427	17	AQ075054	AQ075054 CIT-HSP-2
c 268	17	1.7	312	9	AI031510	AI031510 16H8M Xen	c 341	17	1.7	427	17	AQ845498	AQ845498 LMAJFV1.1
c 269	17	1.7	313	9	AI511375	AI511375 UI-R-C3-s	c 342	17	1.7	427	17	BH613795	BH613795 SALK.0349
c 270	17	1.7	314	9	AA774997	AA774997 ae84f09.s	c 343	17	1.7	428	14	BQ629594	BQ629594 saq04a03
c 271	17	1.7	316	9	AA631221	AA631221 nq80b02.8	c 344	17	1.7	431	10	AW641799	AW641799 cml1e04.w
c 272	17	1.7	318	9	AI249676	AI249676 qx50f11.x	c 345	17	1.7	434	9	AI165361	AI165361 A082p22u
c 273	17	1.7	322	13	BJ499046	BJ499046 BU499046	c 346	17	1.7	434	14	BQ451614	BQ451614 PESToab0
c 274	17	1.7	324	14	BQ455252	BQ455252 ke11b12.Y	c 347	17	1.7	436	10	AW326143	AW326143 18298 MAR
c 275	17	1.7	328	10	BB378800	BB378800 BB378800	c 348	17	1.7	436	17	AQ005448	AQ005448 CIT-HSP-2
c 276	17	1.7	329	14	BQ455106	BQ455106 ke18e02.Y	c 349	17	1.7	438	9	AA730822	AA730822 nw49e05.s
c 277	17	1.7	329	17	CNS00UDG	AL090850 Arabidops	c 350	17	1.7	438	9	AI167138	AI167138 O08a07.x
c 278	17	1.7	332	14	Z45335	Z45335 HSC2MH071.n	c 351	17	1.7	442	9	AA783612	AA783612 Ccd1a1.r
c 279	17	1.7	334	13	BJ059324	BJ059324 BU059324	c 352	17	1.7	443	9	AI356577	AI356577 QY15g08.x
c 280	17	1.7	337	17	AQ591086	AQ591086 HS 5391.B	c 353	17	1.7	444	14	BQ129332	BQ129332 i3j34f08.Y
c 281	17	1.7	341	10	BE072577	BE072577 PM0-BT054	c 354	17	1.7	444	14	AQ456916	AQ456916 HS 5153.A
c 282	17	1.7	343	13	BM16501	BM16501 k15b04.Y	c 355	17	1.7	445	10	BE606644	BE606644 WHE0901.F
c 283	17	1.7	346	13	BM320163	BM320163 re8Sh11.Y	c 356	17	1.7	445	12	BF911135	BF911135 PM1-UT006
c 284	17	1.7	349	14	BQ283143	BQ283143 WHE3086.F	c 357	17	1.7	446	9	AI458373	AI458373 t394e12.x
c 285	17	1.7	350	12	BF370475	BF370475 QV0-FN006	c 358	17	1.7	446	9	AA542638	AA542638 fa08e01.r
c 286	17	1.7	350	17	AZ315331	AZ315331 IM0032F05	c 359	17	1.7	447	9	AA212259	AA212259 mu178b04.r
c 287	17	1.7	351	13	B1816330	B1816330 PHEStoaa3	c 360	17	1.7	448	10	AV874288	AV874288 AV874288
c 288	17	1.7	352	14	BQ282957	BQ282957 WHE3084.B	c 361	17	1.7	449	12	BF250424	BF250424 pa98h11.Y
c 289	17	1.7	353	9	AI974661	AI974661 T1131166_	c 362	17	1.7	450	10	AW159469	AW159469 za99f05.x
c 290	17	1.7	353	17	BH267730	BH267730 CH230-215	c 363	17	1.7	451	13	BI743101	BI743101 kx38f10.Y
c 291	17	1.7	356	13	BM403451	BM403451 zam3369.Z	c 364	17	1.7	451	17	AZ123749	AZ123749 RPCI-23-4
c 292	17	1.7	358	9	AA639002	AA639002 n8o1e07.s	c 365	17	1.7	451	17	AQ130356	AQ130356 HS 3014.A
c 293	17	1.7	358	12	BF868657	BF868657 t13-ET011	c 366	17	1.7	452	10	AW088472	AW088472 xd27d03.x
c 294	17	1.7	358	17	BH858474	BH858474 B5 5900d	c 367	17	1.7	452	17	B97017	B97017 F1511TFB IG
c 295	17	1.7	360	9	AV191206	AV191206 AV191206	c 368	17	1.7	454	12	BG018385	BG018385 daa23f09.
c 296	17	1.7	360	9	AV193616	AV193616 AV193616	c 369	17	1.7	454	17	AQ457675	AQ457675 HS 5127.B
c 297	17	1.7	360	14	C39347	C39347 C39347 Yuji	c 370	17	1.7	456	9	AU037199	AU037199 AU037199
c 298	17	1.7	366	9	AI596369	AI596369 me61d11.x	c 371	17	1.7	456	14	BQ562226	BQ562226 H4074G09-

C 372	17	1.7	457	9	AA819830	AA819830 UI-R-A0-a	445	17	1.7	523	10	AW642062	AW642062 cm14e07.w
373	17	1.7	457	9	AI974580	AI974580 T113030e	446	17	1.7	523	13	BJ174044	BJ174044
374	17	1.7	458	10	AQ518425	AQ518425 HS 5101.A	C 447	17	1.7	523	14	BQ457070	BQ457070 ke34e03.y
375	17	1.7	460	10	BE326460	BE326460 BW4D08.x	C 448	17	1.7	525	13	BI591864	BI591864 RH07665.5
C 376	17	1.7	460	13	BI554530	BI554530 603235660	C 449	17	1.7	527	13	BM388382	BM388382 UI-R-CN1-
C 377	17	1.7	460	17	AZ235235	AZ235235 RPCI-23-8	C 450	17	1.7	528	10	AW852541	AW852541 PM1-CT024
C 378	17	1.7	461	9	AA036753	AA036753 zk31f04.r	451	17	1.7	528	12	BG363904	BG363904 dc72b08.y
C 379	17	1.7	462	10	AW665386	AW665386 bi90b03.x	452	17	1.7	528	12	BF325329	BF325329 su32c07.y
380	17	1.7	462	14	N68492	N68492 za14h04.si	C 453	17	1.7	528	17	TA240D09Q	TA240D09Q
381	17	1.7	466	9	AA680607	AA680607 SMOVL3CAN	C 454	17	1.7	529	9	AI2333785	AI2333785 T. brucei
382	17	1.7	467	17	AQ331702	AQ331702 HS 5011.A	C 455	17	1.7	529	17	BH256826	BH256826 CH230-2473
C 383	17	1.7	468	9	AI079328	AI079328 o236h02.x	C 456	17	1.7	529	17	BH259406	BH259406 CH230-239E
C 384	17	1.7	468	9	AA261861	AA261861 zg18h01.r	C 457	17	1.7	531	9	AI11934	AI11934 EST240228
385	17	1.7	469	12	BF549221	BF549221 UI-R-A0-a	458	17	1.7	531	12	BF215657	BF215657 601881136
C 386	17	1.7	469	17	B58350	B58350 CIT-HSP-201	459	17	1.7	532	10	AV604646	AV604646 AV604646
387	17	1.7	470	13	BI168657	BI168657 RE09489.5	460	17	1.7	532	17	AZ020835	AZ020835 RPCI-23-3
C 388	17	1.7	470	17	AQ226728	AQ226728 HS 2023.B	461	17	1.7	533	9	AI693169	AI693169 wg68d02.x
C 389	17	1.7	471	9	AB033121	AB033121 AB033121	462	17	1.7	533	10	AW552896	AW552896 AV552896
390	17	1.7	471	10	BE251903	BE251903 601107550	C 463	17	1.7	533	10	AW626168	AW626168 xq62b12.x
391	17	1.7	471	12	BG893270	BG893270 daa96b09.	464	17	1.7	533	17	AZ701136	AZ701136 RPCI-23-2
392	17	1.7	476	9	AA485609	AA485609 zx90g06.r	465	17	1.7	534	12	BG613244	BG613244 602641103
393	17	1.7	476	17	AQ492951	AQ492951 HS 5215.B	C 466	17	1.7	535	12	BG813587	BG813587 daif40f12.
C 394	17	1.7	478	9	AI692611	AI692611 wg69h06.x	C 467	17	1.7	537	14	BQ273095	BQ273095 sa01sh11.
C 395	17	1.7	478	14	BQ457134	BQ457134 ke35c07.y	C 468	17	1.7	537	14	C85593	C85593 C85593 Mous
C 396	17	1.7	478	17	AZ522856	AZ522856 212PB03	C 469	17	1.7	537	17	AZ852370	AZ852370 2M0155M20
397	17	1.7	479	13	BJ196840	BJ196840 BJ196840	470	17	1.7	537	17	AQ415076	AQ415076 RPCI-11-1
398	17	1.7	480	10	AW907895	AW907895 ur94g02.y	471	17	1.7	539	12	BG023362	BG023362 dg40e07.x
C 399	17	1.7	480	13	BM567674	BM567674 sak77c11.	C 472	17	1.7	541	9	AI959628	AI959628 fcl2b03.x
C 400	17	1.7	481	17	BH325153	BH325153 CH230-451	C 473	17	1.7	541	13	BJ053741	BJ053741 BJ053741
C 401	17	1.7	482	12	BF939572	BF939572 7047a06.x	474	17	1.7	541	13	AJ053741	AJ053741 BJ053741
C 402	17	1.7	484	10	AV849884	AV849884 AV849884	C 475	17	1.7	541	13	AJ053741	AJ053741 BJ053741
C 403	17	1.7	484	17	AQ619709	AQ619709 HS 5185.A	C 476	17	1.7	542	13	BM608588	BM608588 170006591
404	17	1.7	485	17	AQ368629	AQ368629 HS 5038.A	C 477	17	1.7	543	13	BI578958	BI578958 RE72912.5
C 405	17	1.7	486	13	BM122098	BM122098 10505E04-	C 478	17	1.7	545	14	BQ456234	BQ456234 ke28c01.y
C 406	17	1.7	488	10	AW291937	AW291937 UI-H-B13	C 479	17	1.7	545	17	BH095862	BH095862 RPCI-23-9
C 407	17	1.7	488	12	BF600292	BF600292 264938.NA	C 480	17	1.7	546	10	AV665672	AV665672 AV665672
C 408	17	1.7	489	10	AW523387	AW523387 UI-R-B00-	C 481	17	1.7	546	14	BM702640	BM702640 UI-R-CK1-
C 409	17	1.7	489	17	B47635	B47635 CIT-HSP-363	482	17	1.7	549	10	AW921615	AW921615 EST352919
C 410	17	1.7	490	10	BB854872	BB854872 BB854872	483	17	1.7	549	13	BI846194	BI846194 fq79g04.y
C 411	17	1.7	490	17	AQ932649	AQ932649 RPCI-23-3	484	17	1.7	550	13	BQ456807	BQ456807 ke31c00.y
C 412	17	1.7	491	14	BQ273392	BQ273392 UI-H-C00-	C 485	17	1.7	550	14	BQ456807	BQ456807 ke31c00.y
C 413	17	1.7	492	12	BG234811	BG234811 dab64c10.	C 486	17	1.7	550	17	BH876507	BH876507 hr31e06.b
C 414	17	1.7	493	10	AV851209	AV851209 AV851209	C 487	17	1.7	550	17	AQ340692	AQ340692 RPCI-11-3
C 415	17	1.7	493	12	BF010373	BF010373 ss98h10.y	C 488	17	1.7	552	17	AQ831889	AQ831889 HS 2066.B
C 416	17	1.7	495	10	AV440069	AV440069 AV440069	489	17	1.7	553	13	BM269658	BM269658 saK02f03
C 417	17	1.7	498	10	BE148799	BE148799 CM4-HT024	C 490	17	1.7	553	14	BM986667	BM986667 EST594261
C 418	17	1.7	498	10	BE449104	BE449104 ut52e04.y	C 491	17	1.7	553	14	BQ455351	BQ455351 ke12f04.y
C 419	17	1.7	504	13	BI634810	BI634810 RH39049.5	C 492	17	1.7	554	13	BI189003	BI189003 BJ189003
C 420	17	1.7	505	14	BQ451649	BQ451649 PFEST0ab0	C 493	17	1.7	554	14	BQ455913	BQ455913 ke24c01.y
C 421	17	1.7	505	17	AZ383966	AZ383966 1M0141L17	C 494	17	1.7	555	17	AZ112079	AZ112079 RPCI-23-4
C 422	17	1.7	506	12	BG050107	BG050107 PM1.66.G0	C 495	17	1.7	556	9	AI175578	AI175578 EST219133
C 423	17	1.7	507	17	AZ488795	AZ488795 1M0315FF17	C 496	17	1.7	556	14	BQ456174	BQ456174 ke27d02.y
C 424	17	1.7	507	17	AZ930600	AZ930600 474.dhz56	C 497	17	1.7	557	13	BJ179654	BJ179654 BJ179654
C 425	17	1.7	508	10	AW732686	AW732686 bb11b12.y	498	17	1.7	557	17	AQ745793	AQ745793 HS 2272.A
C 426	17	1.7	509	14	RI6858	RI6858 yf85g01.r1	C 499	17	1.7	558	10	BE145224	BE145224 CM3-HT019
C 427	17	1.7	509	17	AQ319729	AQ319729 RPCI11-10	C 500	17	1.7	558	14	BQ285592	BQ285592 faa51g10.
C 428	17	1.7	510	9	AA624724	AA624724 vb87d05.r	501	17	1.7	560	9	AL588017	AL588017 AL588017
C 429	17	1.7	513	10	AW556590	AW556590 sl06g11.y	C 502	17	1.7	562	14	BQ455450	BQ455450 ke14a04.y
C 430	17	1.7	515	12	BG139419	BG139419 EST479861	C 503	17	1.7	562	14	BQ456908	BQ456908 ke32e10.y
C 431	17	1.7	515	12	BG139670	BG139670 EST480028	C 504	17	1.7	562	14	BQ457137	BQ457137 ke35c10.y
C 432	17	1.7	515	13	BI243071	BI243071 RE40619.5	C 505	17	1.7	563	12	BF554893	BF554893 UI-R-E0-c
C 433	17	1.7	515	13	BI301595	BI301595 UI-R-DL0-	C 506	17	1.7	563	14	BQ457407	BQ457407 ke38f08.y
C 434	17	1.7	516	10	BE292505	BE292505 601058010	C 507	17	1.7	563	14	BQ457423	BQ457423 ke38h06.y
C 435	17	1.7	517	9	AI543025	AI543025 SD09591.5	C 508	17	1.7	563	17	AZ454444	AZ454444 1M0256H24
C 436	17	1.7	517	10	BE663192	BE663192 144201.NA	C 509	17	1.7	564	14	BQ563712	BQ563712 gl05h08.y
C 437	17	1.7	517	14	BQ457337	BQ457337 ke37h03.y	C 510	17	1.7	565	14	BQ455527	BQ455527 ke13g04.y
C 438	17	1.7	518	9	AA947873	AA947873 ok21h03.s	C 511	17	1.7	565	14	BQ456025	BQ456025 ke25e05.y
C 439	17	1.7	518	12	BF611895	BF611895 de89f04.y	C 512	17	1.7	565	14	BQ456601	BQ456601 ke40g12.y
C 440	17	1.7	518	17	CNS00V2J	AL091753 Arabidops	C 513	17	1.7	565	14	BQ456974	BQ456974 ke33d03.y
C 441	17	1.7	518	17	AQ402546	AQ402546 HS 5054.A	C 514	17	1.7	565	14	BQ457082	BQ457082 ke33f04.y
C 442	17	1.7	519	17	AQ425594	AQ425594 CITBI-EI-	C 515	17	1.7	566	14	BQ455285	BQ455285 ke11f02.y
C 443	17	1.7	522	9	AI232613	AI232613 EST229301	C 516	17	1.7	566	17	AQ251509	AQ251509 T6G4-SP6.
C 444	17	1.7	522	10	AW852543	AW852543 PM1-CT024	C 517	17	1.7	567	10	AV679894	AV679894 AV679894

C 518	17	1.7	568	14	BQ454885	BQ454885	ke15g11.y	C 591	17	1.7	629	12	BF635500	BF635500	NF080A01D
C 519	17	1.7	568	14	BQ577311	BQ577311	PfESToab1	592	17	1.7	629	12	BF635500	BF635500	NF080A01D
C 520	17	1.7	568	14	AZ093524	AZ093524	RPCI-23-4	593	17	1.7	629	12	BF635500	BF635500	NF080A01D
C 521	17	1.7	569	13	BM093998	BM093998	sah24c06.y	594	17	1.7	631	10	AI109545	AI109545	GH08770.5
C 522	17	1.7	569	14	BQ455549	BQ455549	ke20a04.y	595	17	1.7	631	10	AI109545	AI109545	GH08770.5
C 523	17	1.7	569	14	BQ455549	BQ455549	ke20a04.y	595	17	1.7	631	10	AI109545	AI109545	GH08770.5
C 524	17	1.7	570	12	BQ456624	BQ456624	PfESToab3	596	17	1.7	631	10	AI109545	AI109545	GH08770.5
C 525	17	1.7	570	12	BQ456624	BQ456624	PfESToab3	596	17	1.7	631	10	AI109545	AI109545	GH08770.5
C 526	17	1.7	571	17	BQ456624	BQ456624	PfESToab3	597	17	1.7	632	12	BG525671	BG525671	52-34 Ste
C 527	17	1.7	571	17	BQ456624	BQ456624	PfESToab3	598	17	1.7	632	12	BG525671	BG525671	52-34 Ste
C 528	17	1.7	573	10	BQ456624	BQ456624	PfESToab3	599	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 529	17	1.7	574	12	BQ456624	BQ456624	PfESToab3	600	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 530	17	1.7	575	10	BQ456624	BQ456624	PfESToab3	601	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 531	17	1.7	576	10	BQ456624	BQ456624	PfESToab3	602	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 532	17	1.7	576	10	BQ456624	BQ456624	PfESToab3	603	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 533	17	1.7	577	13	BQ456624	BQ456624	PfESToab3	604	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 534	17	1.7	577	13	BQ456624	BQ456624	PfESToab3	605	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 535	17	1.7	577	13	BQ456624	BQ456624	PfESToab3	606	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 536	17	1.7	579	9	AU019429	AU019429	AW174020	607	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 537	17	1.7	579	10	AW174020	AW174020	AW174020	608	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 538	17	1.7	581	13	BI840514	BI840514	f875b03.y	609	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 539	17	1.7	581	17	BH350256	BH350256	CH230-198	610	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 540	17	1.7	582	17	BQ456624	BQ456624	PfESToab3	611	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 541	17	1.7	583	14	BM986666	BM986666	EST394260	612	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 542	17	1.7	583	14	BQ454932	BQ454932	ke16d04.y	613	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 543	17	1.7	583	14	BQ454932	BQ454932	ke16d04.y	614	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 544	17	1.7	583	14	BQ454932	BQ454932	ke16d04.y	615	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 545	17	1.7	583	14	BQ454932	BQ454932	ke16d04.y	616	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 546	17	1.7	583	14	BQ454932	BQ454932	ke16d04.y	617	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 547	17	1.7	584	10	BE210610	BE210610	so50h10.y	618	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 548	17	1.7	584	10	BE210610	BE210610	so50h10.y	619	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 549	17	1.7	585	17	AZ0930920	AZ0930920	RPCI-23-3	620	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 550	17	1.7	585	17	B22267	B22267	F18B7TR IGF	621	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 551	17	1.7	587	10	AV859543	AV859543	AV859543	622	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 552	17	1.7	587	10	AV859543	AV859543	AV859543	623	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 553	17	1.7	587	12	BG526852	BG526852	40-59 Ste	624	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 554	17	1.7	587	13	BI715210	BI715210	ic30c04.y	625	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 555	17	1.7	587	13	BI715210	BI715210	ic30c04.y	626	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 556	17	1.7	589	14	BQ455533	BQ455533	ke19g11.y	627	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 557	17	1.7	589	14	BQ455533	BQ455533	ke19g11.y	628	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 558	17	1.7	589	14	BQ455533	BQ455533	ke19g11.y	629	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 559	17	1.7	589	14	BQ455533	BQ455533	ke19g11.y	630	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 560	17	1.7	593	9	AA850598	AA850598	EST193366	631	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 561	17	1.7	594	13	AI103948	AI103948	EST123237	632	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 562	17	1.7	595	14	BM776425	BM776425	fy24f06.y	633	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 563	17	1.7	595	14	BM776425	BM776425	fy24f06.y	634	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 564	17	1.7	597	17	BH784335	BH784335	fzm0013f0	635	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 565	17	1.7	598	17	BH784335	BH784335	fzm0013f0	636	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 566	17	1.7	599	10	AW562578	AW562578	660066F03	637	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 567	17	1.7	599	17	AQ003687	AQ003687	CPG0332B	638	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 568	17	1.7	599	17	CI22A1	CI22A1	AJ226956	639	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 569	17	1.7	600	10	AW421413	AW421413	fj91a07.y	640	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 570	17	1.7	602	12	BG525536	BG525536	48-80 Ste	641	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 571	17	1.7	602	13	BI633124	BI633124	SD27115.5	642	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 572	17	1.7	604	12	BE823537	BE823537	BM000021A	643	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 573	17	1.7	606	17	AQ393025	AQ393025	CITBI-EI-	644	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 574	17	1.7	607	10	AV861080	AV861080	AV861080	645	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 575	17	1.7	607	10	AV861080	AV861080	AV861080	646	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 576	17	1.7	607	10	AV861080	AV861080	AV861080	647	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 577	17	1.7	607	12	EG710479	EG710479	pglin.pk0	648	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 578	17	1.7	609	10	AW671599	AW671599	IG1_348.F	649	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 579	17	1.7	612	17	AZ762041	AZ762041	IM0556N10	650	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 580	17	1.7	613	12	BF239180	BF239180	601905580	651	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 581	17	1.7	616	13	BI826773	BI826773	603077258	652	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 582	17	1.7	616	13	BM239182	BM239182	K0530C10-	653	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 583	17	1.7	616	17	AZ070892	AZ070892	RPCI-23-3	654	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 584	17	1.7	618	9	AI134175	AI134175	GH1556.5	655	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 585	17	1.7	621	12	EG709984	EG709984	pglin.pk0	656	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 586	17	1.7	623	17	DR8M23S	DR8M23S	AL742772	657	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 587	17	1.7	625	12	BG525522	BG525522	50-77 Ste	658	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 588	17	1.7	625	17	AZ439966	AZ439966	IM0330N17	659	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 589	17	1.7	626	17	AQ978056	AQ978056	RPCI-23-3	660	17	1.7	633	12	BG525671	BG525671	52-34 Ste
C 590	17	1.7	627	17	BH760341	BH760341	BMBAC312D	661	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								662	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								663	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								664	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								665	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								666	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								667	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								668	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								669	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								670	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								671	17	1.7	633	12	BG525671	BG525671	52-34 Ste
								672	17	1.7	633	12			

C 664	17	1.7	693	11	AK016337	Mus muscu	C 737	17	1.7	792	14	BO782146	BO782146	UI-RF0-
C 665	17	1.7	695	12	BG744049	602722829	738	17	1.7	796	10	BE131064	BE131064	L48-1014T
C 666	17	1.7	695	13	BI204132	EST522172	C 739	17	1.7	798	12	BG431308	BG431308	602499884
C 667	17	1.7	695	14	BQ575153	UI-H-EZ1-	740	17	1.7	798	13	BI825705	BI825705	603072690
C 668	17	1.7	695	14	BQ990952	QGF21122.	C 741	17	1.7	801	17	BH261954	BH261954	CH230-761
C 669	17	1.7	696	12	BF116218	7n79B04.x	742	17	1.7	802	12	BF571948	BF571948	602078266
C 670	17	1.7	698	17	AG180368	Pan trogl	C 743	17	1.7	809	9	AA768843	AA768843	n275805.s
C 671	17	1.7	698	17	AQ487070	RFC1-11-2	744	17	1.7	816	13	BI766386	BI766386	603052627
C 672	17	1.7	699	12	BG636315	SD13953.5	745	17	1.7	817	10	BE270238	BE270238	601186033
C 673	17	1.7	699	17	AZ726406	RFC1-24-6	C 746	17	1.7	820	17	BH507597	BH507597	BOHG84TR
C 674	17	1.7	700	10	AV874972	AV874972	747	17	1.7	822	14	BQ411248	BQ411248	AGENCOURT
C 675	17	1.7	701	13	BI240114	RE36763.5	748	17	1.7	823	13	BM010546	BM010546	603631728
C 676	17	1.7	703	17	AZ838199	2M0133J18	749	17	1.7	826	17	AQ745631	AQ745631	HS 3273.A
C 677	17	1.7	704	13	BJS16044	BJS16044	C 750	17	1.7	828	12	BG744561	BG744561	602722629
C 678	17	1.7	705	13	BI226660	602951681	751	17	1.7	828	13	BI311353	BI311353	EST531310
C 679	17	1.7	706	10	BE264974	601194081	C 752	17	1.7	829	17	BH539763	BH539763	BOGP94TR
C 680	17	1.7	707	17	BH293189	CH230-115	C 753	17	1.7	831	12	BG744636	BG744636	602722729
C 681	17	1.7	707	17	AG125905	Pan trogl	754	17	1.7	832	17	AZ186671	AZ186671	SP 1007.B
C 682	17	1.7	710	13	BI374883	RE62569.5	755	17	1.7	833	13	BI916561	BI916561	603178476
C 683	17	1.7	710	13	BM592171	170006685	756	17	1.7	839	9	AI068687	AI068687	mgae0003d
C 684	17	1.7	710	17	B72080	CIT-HSP-363	757	17	1.7	840	13	BI462531	BI462531	603205439
C 685	17	1.7	712	13	BM657978	BM657978	758	17	1.7	851	9	AUI25099	AUI25099	AUI25099
C 686	17	1.7	713	13	BI590975	MCA058C04	C 759	17	1.7	851	17	ENTG7130	ENTG7130	ENTG7130
C 687	17	1.7	713	17	AZ994333	2M0279F18	760	17	1.7	852	17	AQ749980	AQ749980	HS 5576.A
C 688	17	1.7	714	17	AZ956917	2M0223B12	761	17	1.7	856	13	BI107092	BI107092	602894514
C 689	17	1.7	717	13	BM58149	MCR050F04	762	17	1.7	862	12	BF977573	BF977573	602147357
C 690	17	1.7	719	13	BM578500	170006871	C 763	17	1.7	864	9	AI789316	AI789316	uk53f09.y
C 691	17	1.7	721	12	BF032937	601455893	764	17	1.7	866	12	BF785983	BF785983	601478239
C 692	17	1.7	722	10	AV850913	AV850913	765	17	1.7	868	12	BF571981	BF571981	602077812
C 693	17	1.7	724	17	BH672553	BOHX235TR	766	17	1.7	877	12	BG031457	BG031457	602298873
C 694	17	1.7	726	12	BG703971	602687076	767	17	1.7	879	12	BF699164	BF699164	602126803
C 695	17	1.7	728	12	BG776861	602664044	768	17	1.7	882	12	BG743090	BG743090	602634225
C 696	17	1.7	728	17	AQ960452	LERF90TR	769	17	1.7	887	9	AA203338	AA203338	zx54n08.f
C 697	17	1.7	729	17	AG186153	AG186153	C 770	17	1.7	890	12	BF247212	BF247212	601857902
C 698	17	1.7	729	10	BE561925	601346653	771	17	1.7	891	12	BF664359	BF664359	602146017
C 699	17	1.7	729	17	BH840362	2M0198B08	C 772	17	1.7	891	17	BH159899	BH159899	ENTRX01TR
C 700	17	1.7	730	17	AZ939224	2M0198B08	773	17	1.7	892	17	AZ541222	AZ541222	ENTGP85TF
C 701	17	1.7	731	10	AV887784	AV887784	774	17	1.7	893	17	AZ530563	AZ530563	ENTBM48TR
C 702	17	1.7	734	12	BG546113	602573529	775	17	1.7	895	9	AL556437	AL556437	AL556437
C 703	17	1.7	735	13	BI226898	602952014	C 776	17	1.7	895	17	AZ551104	AZ551104	ENTGCS9TR
C 704	17	1.7	736	9	AA698330	HL04288.5	777	17	1.7	900	17	AZ530049	AZ530049	ENTBS93TF
C 705	17	1.7	737	17	BH278203	CH230-24E	778	17	1.7	905	12	BF106664	BF106664	601823132
C 706	17	1.7	738	13	BI930626	EST550515	779	17	1.7	908	17	AZ530571	AZ530571	ENTBU54TF
C 707	17	1.7	740	9	AI293274	GH16429.9	780	17	1.7	914	9	AI106683	AI106683	GH06759.5
C 708	17	1.7	740	9	AI587033	AI587033	781	17	1.7	914	12	BE874186	BE874186	601484372
C 709	17	1.7	740	17	BH476015	BH476015	C 782	17	1.7	915	9	AL578692	AL578692	AL578692
C 710	17	1.7	744	14	W27445	W27445	783	17	1.7	916	17	BH149381	BH149381	ENTQK27TF
C 711	17	1.7	746	13	BI461669	603205804	784	17	1.7	917	14	BQ717032	BQ717032	AGENCOURT
C 712	17	1.7	748	12	BE791507	601588841	785	17	1.7	919	14	BQ723759	BQ723759	AGENCOURT
C 713	17	1.7	750	17	AG079502	AG079502	786	17	1.7	921	12	BG178537	BG178537	602328366
C 714	17	1.7	752	10	AV544760	AV544760	787	17	1.7	923	9	AA203659	AA203659	zx58n12.f
C 715	17	1.7	754	12	BF607597	MY1-00053	788	17	1.7	932	13	BI763601	BI763601	603050168
C 716	17	1.7	756	12	BG531305	602559539	789	17	1.7	933	10	BH147091	BH147091	ENTPN75TR
C 717	17	1.7	756	12	BG621857	602646414	790	17	1.7	939	17	BE561026	BE561026	601344634
C 718	17	1.7	766	12	BG587712	EST489487	791	17	1.7	941	17	BG031747	BG031747	602299809
C 719	17	1.7	767	17	AZ695195	RPCI-23-2	C 792	17	1.7	941	17	AZ686088	AZ686088	ENTFW87TR
C 720	17	1.7	767	17	BH040006	BH040006	793	17	1.7	950	12	BG743957	BG743957	602722729
C 721	17	1.7	772	17	AZ989755	2M0273P09	794	17	1.7	950	12	BE965277	BE965277	601659382
C 722	17	1.7	774	9	AJ454980	AJ454980	795	17	1.7	952	10	BE538509	BE538509	601068162
C 723	17	1.7	775	17	AQ749378	HS 5573.A	796	17	1.7	959	12	BF138512	BF138512	601782969
C 724	17	1.7	776	12	BG830544	602767132	C 797	17	1.7	968	17	CNS0435M	AL272371	Tetraodon
C 725	17	1.7	777	9	AJ446862	AJ446862	798	17	1.7	974	14	BQ060869	BQ060869	AGENCOURT
C 726	17	1.7	777	13	BI643077	POX1-E2.S	799	17	1.7	976	12	BG388484	BG388484	602413522
C 727	17	1.7	778	13	BI461648	603206773	800	17	1.7	993	12	BG285474	BG285474	602380446
C 728	17	1.7	778	17	BH419244	BH419244	C 801	17	1.7	993	17	AL190187	AL190187	Tetraodon
C 729	17	1.7	778	17	BH425379	BOGOV43TR	C 802	17	1.7	999	12	CNS02BQ	BF662937	602144729
C 730	17	1.7	779	9	AJ454745	BOGTQ14TR	803	17	1.7	1014	14	BQ056178	BQ056178	AGENCOURT
C 731	17	1.7	780	17	CNS00T88	AJ454745	804	17	1.7	1014	17	CNS03PPY	AL254959	Tetraodon
C 732	17	1.7	782	9	AL638303	tt09C09.x	C 805	17	1.7	1020	12	BG115731	BG115731	602317016
C 733	17	1.7	784	12	BF965634	602276718	806	17	1.7	1025	14	BQ050700	BQ050700	AGENCOURT
C 734	17	1.7	785	17	AQ872094	nbe0046H	C 807	17	1.7	1032	12	BG752898	BG752898	602732545
C 735	17	1.7	786	14	BQ429272	AGENCOURT	C 808	17	1.7	1043	17	AG159941	AG159941	Pan trogl
C 736	17	1.7	787	17	BH421909	BOHQA81TR	809	17	1.7	1044	17	AZ691539	AZ691539	ENTL44TR

C 810	17	1.7	1054	17	CNS033WM	AL226697 Tetraodon	C 883	16	1.6	17	AZ627272	AZ627272 1M0469C03
C 811	17	1.7	1058	17	AZ209307	SP 0101 A	884	16	1.6	216	9	AA047149 z1K74F03.r
C 812	17	1.7	1072	14	BQ436660	AGENCOURT	885	16	1.6	221	10	AA047149 z1K74F03.r
C 813	17	1.7	1079	17	CNS078PB	AL433917 T3 end of	886	16	1.6	221	10	AV316744 AV316744
C 814	17	1.7	1088	17	CNS01461	AL103764 Drosophila	887	16	1.6	221	12	BF327590 WRO-BN011
C 815	17	1.7	1092	14	BM912276	BM912276 AGENCOURT	888	16	1.6	223	12	BF327590 WRO-BN011
C 816	17	1.7	1101	17	CNS000F6	AL052843 Drosophila	889	16	1.6	223	12	BF327590 WRO-BN011
C 817	17	1.7	1101	17	CNS056TV	AL323788 Tetraodon	890	16	1.6	224	14	BF327590 WRO-BN011
C 818	17	1.7	1101	17	CNS050Q6	AL346983 Tetraodon	891	16	1.6	225	14	BF327590 WRO-BN011
C 819	17	1.7	1148	13	BI561805	BI561805 Tetraodon	892	16	1.6	225	14	BF327590 WRO-BN011
C 820	17	1.7	1196	12	BE786921	BE786921 601477792	893	16	1.6	226	14	BF327590 WRO-BN011
C 821	17	1.7	1214	13	BM450200	BM450200 AGENCOURT	894	16	1.6	227	10	BF327590 WRO-BN011
C 822	17	1.7	1255	12	BG847688	BG847688 1024018F1	895	16	1.6	228	10	BF327590 WRO-BN011
C 823	17	1.7	1465	11	BC001557	BC001557 Homo sapi	896	16	1.6	228	10	BF327590 WRO-BN011
C 824	17	1.7	1492	13	BI905819	BI905819 603062779	897	16	1.6	228	10	BF327590 WRO-BN011
C 825	17	1.7	1622	12	BG333619	BG333619 602460506	898	16	1.6	231	13	BM644704
C 826	17	1.7	1677	11	BC008463	BC008463 Homo sapi	899	16	1.6	232	9	AI101061
C 827	17	1.7	1865	11	BC033014	BC033014 Homo sapi	900	16	1.6	232	10	AV378076
C 828	17	1.7	1913	12	BG029237	BG029237 602292451	901	16	1.6	232	10	AV378076
C 829	16	1.6	83	14	D12012	D12012 HUM0005145	902	16	1.6	233	9	AV280040
C 830	16	1.6	83	14	D12013	D12013 HUM0005146	903	16	1.6	233	9	AV280040
C 831	16	1.6	97	9	AI453376	AI453376 t337e01.x	904	16	1.6	233	12	BG315545
C 832	16	1.6	99	10	AV957678	AV957678 AV957678	905	16	1.6	234	9	AV283173
C 833	16	1.6	112	13	BM255274	BM255274 516964 MA	906	16	1.6	235	14	BM896396
C 834	16	1.6	121	14	BQ980017	BQ980017 QH19014.Y	907	16	1.6	236	10	BE115330
C 835	16	1.6	123	10	AW603298	AW603298 RC1-CN001	908	16	1.6	237	10	AV352765
C 836	16	1.6	138	12	BF270504	BF270504 GA_Eb000	909	16	1.6	237	10	AW404339
C 837	16	1.6	139	12	BG063819	BG063819 H301A10-	910	16	1.6	238	9	AV282534
C 838	16	1.6	142	9	AA786532	AA786532 m3a09a1.r	911	16	1.6	238	17	BH721259
C 839	16	1.6	147	10	AW813716	AW813716 RC3-ST019	912	16	1.6	239	9	AA054916
C 840	16	1.6	147	13	BI245272	BI245272 949027A09	913	16	1.6	239	9	AA054916
C 841	16	1.6	152	9	AU254210	AU254210 AU254210	914	16	1.6	240	9	AA353180
C 842	16	1.6	152	12	BF073492	BF073492 220206 MA	915	16	1.6	240	12	BH843012
C 843	16	1.6	152	10	AQ200890	AQ200890 RPI111-62	916	16	1.6	241	10	BQ320734
C 844	16	1.6	162	17	BH857668	BH857668 SALK_0163	917	16	1.6	241	10	BQ320734
C 845	16	1.6	163	17	AL770008	AL770008 Arabidops	918	16	1.6	241	10	BH84621
C 846	16	1.6	166	12	BE824540	BE824540 C0501A08	919	16	1.6	241	14	BU019566
C 847	16	1.6	170	17	B89920	B89920 CIT-HSP-217	920	16	1.6	243	10	AV340726
C 848	16	1.6	171	14	BQ974498	BQ974498 QH15005.	921	16	1.6	243	14	BU016802
C 849	16	1.6	172	10	AV380970	AV380970 AV380970	922	16	1.6	244	12	BG001036
C 850	16	1.6	172	17	BH412959	BH412959 1007029H1	923	16	1.6	244	14	BQ871145
C 851	16	1.6	172	17	BH412959	BH412959 1007029H1	924	16	1.6	244	14	BQ871145
C 852	16	1.6	175	10	BQ039886	BQ039886 BQ039886	925	16	1.6	244	17	AZ240676
C 853	16	1.6	175	10	BE467206	BE467206 hz63a08.x	926	16	1.6	245	17	AZ240676
C 854	16	1.6	175	13	BG981683	BG981683 MR3-CN014	927	16	1.6	246	10	AV838927
C 855	16	1.6	177	10	AW994704	AW994704 RC1-BN003	928	16	1.6	246	10	BQ048783
C 856	16	1.6	178	10	AW786769	AW786769 120270 MA	929	16	1.6	246	13	BI200521
C 857	16	1.6	178	13	BG996646	BG996646 PM0-HT091	930	16	1.6	247	9	AA634877
C 858	16	1.6	184	10	AW369462	AW369462 RC0-BN000	931	16	1.6	247	14	BU023018
C 859	16	1.6	185	10	BB244210	BB244210 BB244210	932	16	1.6	248	9	AV284306
C 860	16	1.6	185	12	BG093690	BG093690 mab42c12.	933	16	1.6	248	14	F02957
C 861	16	1.6	189	10	B5333465	B5333465 B5333465	934	16	1.6	249	9	AV281976
C 862	16	1.6	189	10	B5333465	B5333465 B5333465	935	16	1.6	249	14	BQ911698
C 863	16	1.6	192	14	BQ985255	BQ985255 Q56F08.Y	936	16	1.6	250	9	AA378757
C 864	16	1.6	192	14	N56521	N56521 LX1254F Hum	937	16	1.6	250	10	AA378757
C 865	16	1.6	194	12	BG689903	BG689903 338226 BA	938	16	1.6	250	14	BQ703139
C 866	16	1.6	195	10	BQ037967	BQ037967 BQ037967	939	16	1.6	250	10	AW864574
C 867	16	1.6	197	17	AZ1133260	AZ1133260 RPI1-23-9	940	16	1.6	251	9	AA090325
C 868	16	1.6	199	10	AV347152	AV347152 AV347152	941	16	1.6	251	14	BM855216
C 869	16	1.6	200	10	AW325342	AW325342 16434 MAR	942	16	1.6	251	14	BM855216
C 870	16	1.6	201	9	AI926497	AI926497 w045601.x	943	16	1.6	256	10	BQ048063
C 871	16	1.6	201	9	AA125843	AA125843 cgh0134.x	944	16	1.6	257	10	AV354539
C 872	16	1.6	202	10	AW374613	AW374613 MR1-CT005	945	16	1.6	257	10	BB011133
C 873	16	1.6	205	10	AW662998	AW662998 hb83h09.y	946	16	1.6	257	10	BB011133
C 874	16	1.6	207	10	BQ201027	BQ201027 BB201027	947	16	1.6	257	10	BB150627
C 875	16	1.6	208	14	BQ202994	BQ202994 AGENCOURT	948	16	1.6	257	14	F02250
C 876	16	1.6	209	9	AI646472	AI646472 VY37G12.x	949	16	1.6	258	14	BQ451014
C 877	16	1.6	209	13	BM225219	BM225219 K0208C06-	950	16	1.6	258	14	BU015991
C 878	16	1.6	209	14	T30799	T30799 EST2863 Hu	951	16	1.6	258	14	BU016786
C 879	16	1.6	209	14	T30799	T30799 EST2863 Hu	952	16	1.6	259	9	AV285604
C 880	16	1.6	211	10	BE187111	BE187111 NKNV.159	953	16	1.6	259	14	BU018174
C 881	16	1.6	212	10	AV364654	AV364654 AV364654	954	16	1.6	260	10	BB349554
C 882	16	1.6	213	17	BH023760	BH023760 BG02096 D	955	16	1.6	260	14	BU018047


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BASE COUNT      63 a      61 c      49 g      29 t
ORIGIN
Query Match      2.1%; Score 20; DB 12; Length 202;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 TAACCAAAAAAATGCACAA 292
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Db 92 TAACCAAAAAAATGCACAA 111

RESULT 3
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LOCUS 2x60d08.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795855
DEFINITION 5' similar to gb:U13680 L-LACTATE DEHYDROGENASE X CHAIN (HUMAN);,
      mRNA sequence.
ACCESSION AA460603
VERSION AA460603.1 GI:2185723
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
      Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
      Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
      ,T., Waterston,K. and Wilson,R.
      WashU-Merck EST Project 1997
      Unpublished (1997)
      Contact: Wilton RK
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: est@watson.wustl.edu
      This clone is available royalty-free through LNL; contact the
      IMAGE Consortium (info@image.llnl.gov) for further information.
      Seq primer: -28ml3 rev2 ET from Amersham
      High quality sequence stop: 323.
      mRNA sequence.
FEATURES
      source
      1..578
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      /db_xref="GDB:6039437"
      /db_xref="taxon:9606"
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      /clone_lib="Soares_testis_NHT"
      /sex="male"
      /lab_host="DH10B"
      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
      was prepared from mRNA obtained from Clontech Laboratories
      , Inc., and primed with a Not I - oligo(dT) primer [5'
      TGTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'].
      Double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization to Cot5, and was
      constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      165 a      99 c      142 g      172 t
ORIGIN
Query Match      2.1%; Score 20; DB 9; Length 578;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGGTGATTC 566
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Db 341 ATTGGAGAACATGGTGATTC 360

RESULT 4
BH554885 580 bp DNA linear GSS 14-DEC-2001
LOCUS BOGDC32TF BOGD Brassica oleracea genomic clone BOGDC32, DNA
DEFINITION sequence.
ACCESSION BH554885
VERSION BH554885.1 GI:17806665
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 580)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOGDC32TR
      Contact: Chris Town
      TIGR
      9712 Medical Center Drive, Rockville, MD 20850, USA.
      Tel: 301-838-3523
      Fax: 301-838-0208
      Email: cdtown@tigr.org
      DNA is from a doubled haploid provided by Tom Osborn.
      Seq primer: TF
      Class: sheared ends.
FEATURES
      source
      1..580
      /organism="Brassica oleracea"
      /strain="TO1000DH3"
      /db_xref="taxon:3712"
      /clone="BOGDC32"
      /clone_lib="BOGD"
      /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
      genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT      191 a      107 c      161 g      121 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 898 GATGAGAGGAGAAATAGAATT 917
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Db 466 GATGAGAGGAGAAATAGAATT 485

RESULT 5
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LOCUS 2x45c06.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795178
DEFINITION 5' similar to gb:U13680 L-LACTATE DEHYDROGENASE X CHAIN (HUMAN);,
      mRNA sequence.
ACCESSION AA453969
VERSION AA453969.1 GI:2167638
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
      Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
      Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
      ,T., Waterston,K. and Wilson,R.
      WashU-Merck EST Project 1997
      Unpublished (1997)
      Contact: Wilton RK
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810

```

Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m13 rev2 EF from Amersham
 High quality sequence stop: 370.

FEATURES

Location/Qualifiers
 1. 583
 /organism="Homo sapiens"
 /db_xref="GDB:6038074"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:795178"
 /sex="male"
 /lab host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 , Inc., and primed with a Not I - Oligo(dT) primer [5',
 TGTTCACCAATCTGAAGTGGGAGCGCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT
 ORIGIN

Query Match 2.1%; Score 20; DB 9; Length 583;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGTGTATTC 566
 Db 154 ATTGGAGAACATGTGTATTC 173

RESULT 6

PT005G13U 592 bp DNA linear GSS 13-JUL-2001
 LOCUS Parametium tetraurelia sequence M05D07u of the end of plasmid
 DEFINITION PT005G13, genomic survey sequence.

ACCESSION AL446361
 VERSION AL446361.1 GI:11121969
 KEYWORDS GSS.
 SOURCE Parametium tetraurelia.
 ORGANISM Parametium tetraurelia.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;

REFERENCE

1 (bases 1 to 592)
 Koller,A.M. and Cohen,J.
 TITLE An indexed genomic library for Parametium complementation cloning
 JOURNAL J. Eukaryot. Microbiol. 47 (1), 1-6 (2000)

REFERENCE

2 (bases 1 to 592)
 Dessen,P., Zagulski,M., Gromadka,R., Plattner,H., Kissmehl,R.,
 Meyer,E., Betermier,M., Schultz,J.E., Linder,J., Pearlman,R.E.,
 Kung,C., Forney,J., Satir,B.H., Van Houten,J.L., Keller,A.M.,
 Froissard,M., Sperling,L. and Cohen,J.
 TITLE Parametium genome survey: a pilot project
 JOURNAL Trends Genet. 17 (6), 306-308 (2001)

REFERENCE

3 (bases 1 to 592)
 Gromadka,R. and Zagulski,M.
 TITLE Random sequencing of the Parametium macronuclear genome
 JOURNAL Unpublished
 REMARK Institute of Biochemistry and Biophysics, Polish Academy of
 Sciences, Warsaw, Poland
 4 (bases 1 to 592)
 Cohen,J. and Sperling,L.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2000) Parametium Genome Survey Project, Centre de

COMMENT

The present survey of the Parametium tetraurelia macronuclear
 genome consists of end sequences of a library of random 4-12 kb
 fragments obtained by Sau3A partial digestion of macronuclear DNA
 cloned in the BamHI site of pBSIKS-. See [4].
 Genes are predicted from matches to other sequences. For more
 information about this sequence or the Parametium Project, see
 http://parametium.cgm.cnr.fr.

FEATURES

Location/Qualifiers
 1. 592
 /organism="Parametium tetraurelia"
 /macronuclear
 /strain="stock d4-2"
 /db_xref="taxon:5888"

BASE COUNT 179 a 92 c 80 g 241 t
 ORIGIN

Query Match 2.1%; Score 20; DB 17; Length 592;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 633 CAACACATATTGTATTCAGA 652
 Db 173 CAACACATATTGTATTCAGA 192

RESULT 7

BQ792707/c

LOCUS

EST 8427 Red Grape berries Lambda Triplex2 Library Vitis vinifera

DEFINITION CDNA clone CM005B02 3', mRNA sequence.

ACCESSION BQ792707

VERSION BQ792707.1

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera.

REFERENCE

AUTHORS

Abbal,P., Agasse,A.,

Agarwal,A., Atanassova,R.,

Barrieu,F.,

Buttore,C., Dedaldecamp,F.,

Delrot,S., Glissant,D.,

Grimplet,J.,

Hamdi,S., Romieu,C. and

Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33893 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1. 607

/organism="Vitis vinifera"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CM005B02"

/clone_lib="Red Grape berries Lambda Triplex2 Library"

/dev_stage="Harvest - 15.5 weeks post-flowering"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2

/Site 1: SfiIA; Site 2: SfiIB; Oriented library"

BASE COUNT 169 a 148 c 128 g 162 t
 ORIGIN

Query Match 2.1%; Score 20; DB 14; Length 607;
 Best Local Similarity 100.0%; Pred. No. 18;

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 AAAAAATGGACAAACAGG 297
    |||||
Db 176 AAAAAATGGACAAACAGG 157

RESULT 8
AI638822/c
LOCUS
DEFINITION
t13202.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2242514 3',
similar to gb:U13680 L-LACTATE DEHYDROGENASE X CHAIN (HUMAN);, mRNA
sequence.
ACCESSION
AI638822
VERSION
AI638822.1 GI:4691056
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 616)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 430.
FEATURES
    source
        1..616
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="lib=NCI CGAP GC6"
            /tissue_type="pooled germ cell tumors"
            /lab_host="DH10B"
            /note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469084-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT
180 a 143 c 91 g 201 t 1 others
ORIGIN
Query Match 2.1%; Score 20; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGCTGATTC 566
    |||||
Db 570 ATTGGAGAACATGCTGATTC 551

RESULT 9
AG148738/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-011A13.TJ, genomic survey
sequence.
ACCESSION
AG148738

```

```

VERSION
KEYWORDS
SOURCE
AG148738.1 GI:16678416
Pan troglodytes male lymphocytes DNA, clone lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-011A13.TJ.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1
AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
BAC end sequences of Library RPCI-43
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 680)
AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
Direct Submission
JOURNAL
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
    source
        1..680
            /organism="Pan troglodytes"
            /db_xref="taxon:9598"
            /clone="RP43-011A13.TJ"
            /sex="male"
            /cell_type="lymphocytes"
            /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT
213 a 124 c 119 g 223 t 1 others
ORIGIN
Query Match 2.1%; Score 20; DB 17; Length 680;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 TTAACCAAAAATGGACAA 291
    |||||
Db 457 TTAACCAAAAATGGACAA 438

RESULT 10
LOCUS
BI827602
DEFINITION
603073568F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165608 5',
mRNA sequence.
ACCESSION
BI827602
VERSION
BI827602.1 GI:15939139
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 713)
AUTHORS
NIH-MGC http://mgs.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM1411 row: 9 column: 17
High quality sequence stop: 711.

FEATURES

source

1. 713
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:515608"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
207 a 114 c 169 g 223 t

BASE COUNT

ORIGIN

Query Match 2.1%; Score 20; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

547 ATTGGAGAACATGGTGATTC 566

Db

211 ATTGGAGAACATGGTGATTC 230

RESULT 11

AW515709/c

LOCUS

DEFINITION AW515709 714 bp mRNA linear EST 03-MAR-2000
hd87c06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2916490 3'
similar to gb:U13680 L-LACTATE DEHYDROGENASE X CHAIN (HUMAN);, mRNA
sequence.

ACCESSION

AW515709

VERSION

AW515709.1 GI:7153791

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonald, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 472.

FEATURES

source

1. 714
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2916490"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonald.

BASE COUNT 220 a 166 c 111 g 215 t 2 others
ORIGIN

Query Match 2.1%; Score 20; DB 10; Length 714;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

547 ATTGGAGAACATGGTGATTC 566

Db

552 ATTGGAGAACATGGTGATTC 533

RESULT 12

BG547106

LOCUS

DEFINITION BG547106 725 bp mRNA linear EST 04-APR-2001
602574310F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4702395 5',
mRNA sequence.

ACCESSION

BG547106

VERSION

BG547106.1 GI:13545771

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1539 row: c column: 04
High quality sequence stop: 724.

FEATURES

source

1. 725
/location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4702395"
/clone_lib="NIH_MGC 77"
/lab host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, G or N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
197 a 136 c 179 g 213 t

BASE COUNT

ORIGIN

Query Match 2.1%; Score 20; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

547 ATTGGAGAACATGGTGATTC 566

|||||

Db 547 ATTGGAGAACATGGTGATTC 566.

RESULT 13
LOCUS BQ797938/c
DEFINITION BQ797938 745 bp mRNA linear EST 30-JUL-2002
DESCRIPTION BQ797938 745 bp mRNA linear EST 30-JUL-2002
ACCESSION BQ797938
VERSION BQ797938.1 GI:22012904
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
1 (bases 1 to 745)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedalchamps, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..745
/organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="RF093E05"
/clone_lib="Ripening stage"
/dev_stage="Ripening stage"
/notes="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco RI
; Site 2: XhoI; Oriented library, construction described
in Generation of ESTs from Grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"
BASE COUNT 186 a 192 c 169 g 198 t
ORIGIN

Query Match 2.1%; Score 20; DB 14; Length 745;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 AAAAAATGGACAAACAGG 297.
Db 114 AAAAAATGGACAAACAGG 95

RESULT 14
LOCUS BQ723296
DEFINITION BQ723296 756 bp mRNA linear EST 08-MAY-2001
DESCRIPTION BQ723296 756 bp mRNA linear EST 08-MAY-2001
ACCESSION BQ723296
VERSION BQ723296.1 GI:14002483
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

FEATURES
source
Location/Qualifiers
1..756
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169698 5",
/clone_lib="NIH_MGC_119"

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10732 row: h column: 07
High quality sequence stop: 755.
Location/Qualifiers
1..756
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4823094"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 194 a 136 c 193 g 233 t
ORIGIN

Query Match 2.1%; Score 20; DB 12; Length 756;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 ATTGGAGAACATGGTGATTC 566
Db 653 ATTGGAGAACATGGTGATTC 672

RESULT 15
LOCUS BI828443
DEFINITION BI828443 774 bp mRNA linear EST 04-OCT-2001
DESCRIPTION BI828443 774 bp mRNA linear EST 04-OCT-2001
ACCESSION BI828443
VERSION BI828443.1 GI:15939993
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1422 row: b column: 03
High quality sequence stop: 772.
Location/Qualifiers
1..774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5169698 5",
/clone_lib="NIH_MGC_119"

```

/tissue type="medulla"
/lab host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH MGC Library."
BASE COUNT      206 a      142 c      189 g      237 t
ORIGIN

```

```

Query Match      2.1%; Score 20; DB 13; Length 774;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      547 ATTGGAGAACATGGTGATTC 566
      |||||
Db      648 ATTGGAGAACATGGTGATTC 667

```

Search completed: July 31, 2003, 11:58:57
Job time : 1863 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 06:49:36 ; Search time 2765 Seconds
(without alignments)
10230.715 Million cell updates/sec

Title: US-09-992-430B-21

Perfect score: 972

Sequence: 1 atgttcaagatacaaaagtc.....ttggacatctggagatcaat 972

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	265.4	27.3	30176	8	SPAC186	AL157811 S.pombe c
C 2	216.4	22.3	1423	1	BACLDHAA	M2305 B.megateriu
C 3	205.2	21.1	10029	1	AE006274	AE006274 Lactococc
C 4	201.2	20.7	11158	1	AE007540	AE007540 Clostridi
C 5	199.4	20.5	948	1	AY098994	AY098994 Clostridi
C 6	185.8	19.1	301450	1	AP003185	AP003185 Clostridi
C 7	183.8	18.9	969	6	AX142689	AX142689 Sequence
C 8	183.8	18.9	969	6	AX143661	AX143661 Sequence
C 9	183.8	18.9	3019	1	AF270315	AF270315 Staphyloc
C 10	183.8	18.9	3019	6	AX145633	AX145633 Sequence
C 11	183.8	18.9	4093	1	AF269753	AF269753 Staphyloc
C 12	183.8	18.9	4093	6	AX145071	AX145071 Sequence
C 13	183.6	18.9	1255	6	AX406983	AX406983 Sequence
C 14	176.6	18.2	1130	1	TMLDHH	X74302 T.maritima
C 15	176.6	18.2	12762	1	AE001823	AE001823 Thermotog
C 16	173.2	17.8	6984	1	AF054824	AF054824 Lactobacil
C 17	171.6	17.7	1260	1	LSU26688	U26688 Lactobacill
C 18	171	17.6	301250	1	AP004830	AP004830 Staphyloc
C 19	169.4	17.4	297850	1	AP003137	AP003137 Staphyloc
C 20	169.4	17.4	341350	1	AP003365	AP003365 Staphyloc
C 21	166.8	17.2	290250	1	AP004822	AP004822 Staphyloc
C 22	166.8	17.2	298050	1	AP003129	AP003129 Staphyloc
C 23	166.8	17.2	349999	1	AP003358	AP003358 Staphyloc
C 24	164.6	16.9	1168	1	LBALDH	M76708 L.casei lac
C 25	164.6	16.9	1364	1	LBALLCT	D12591 L.casei gen
C 26	161.2	16.6	1199	1	BPSC7B	X55119 B. psychros
C 27	157.2	16.2	12584	1	AE006557	AE006557 Streptoco
C 28	156.6	16.1	1260	1	STRLCT	L42474 Streptococc
C 29	156.6	16.1	1292	1	STRLDH	M7545 Streptococc
C 30	155.8	16.0	945	6	E28918	E28918 Lactate deh
C 31	155.8	16.0	1065	6	AX065003	AX065003 Sequence
C 32	155.6	16.0	50734	1	AE014152	AE014152 Streptoco
C 33	155.4	16.0	978	1	LLU78637	U78637 Lactococcu
C 34	155.2	16.0	1086	1	BACLDHRA	M1995 B.caldotena
C 35	155.2	16.0	1244	1	SPR6LDH	AE000336 Streptoco
C 36	155.2	16.0	11614	1	AE008483	AE008483 Streptoco
C 37	155.2	16.0	77743	2	SPNEU1910	AL449932 Streptoco
C 38	154.2	15.9	942	6	AX123294	AX123294 Sequence
C 39	154.2	15.9	224650	1	AL596164	AL596164 Listeria
C 40	154.2	15.9	309400	6	AX127153	AX127153 Sequence
C 41	154.2	15.9	325651	1	AP005283	AP005283 Corynebac
C 42	154.2	15.9	349980	6	AX415067	AX415067 Sequence
C 43	154.2	15.9	349980	6	AX453571	AX453571 Sequence
C 44	153.6	15.8	1368	1	BACLC7LDH	M28336 B.caldotena
C 45	153.6	15.8	5278	6	BD003907	BD003907 Polynucle

ALIGNMENTS

RESULT 1
SPAC186/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

SPAC186
S.pombe chromosome I cosmid c186.
AL157811
AL157811.1 GI:7024417
2-hydroxyacid dehydrogenase; D-isomer specific 2-hydroxyacid
dehydrogenases domain; gene free region; 1-asparaginase precursor;
1-lactate dehydrogenase; mitochondrial transit peptide; pyruvate
decarboxylase; subtelomeric region; Tfi-type LTR; Tfi2-type LTR;
Uncharacterized protein family UPF0016 domain.
Schizosaccharomyces pombe.
Schizosaccharomycetes pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
Schizosaccharomycetales; Schizosaccharomycetaceae;

linear
30176 bp
DNA
PLN 22-FEB-2000

Schizosaccharomyces.
 1 (bases 1 to 30176)
 Wood,V., Rajandream,M.A., Barrell,B.G., Seeger,K. and Harris,D.
 Direct Submission
 Submitted (22-FEB-2000) European Schizosaccharomyces genome
 sequencing project, Sanger Centre, The Wellcome Trust Genome
 Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
 Notes:
 Details of yeast sequencing at the Sanger Centre are available on
 the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/s_pombe/)
 During 1995 to 1996 about 66% of S. pombe chromosome 1 was
 sequenced by the Sanger Centre. The sequencing of the S. pombe
 genome is now being continued with funding from The European
 Commission. Fourteen European sequencing laboratories, including
 the Sanger Centre, are participating in the project.
 Protein coding regions (CDS) have been predicted with the help of
 computer analysis using the GeneFinder program in PomBase (an ACSD
 database) with additional predictions for the branch-acceptor sites
 supplied by the program Sp3splice. CAUTION: It is possible that for
 any individual CDS we may have underestimated or overestimated the
 number of introns/exons or we may not have chosen the correct
 splice donor/acceptor sites.
 CDS are numbered using the following system eg SPBC25H2.01c. SP (S.
 pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
 (complementary strand).
 The more significant matches with motifs in the PROSITE database
 are also included but some of these may be fortuitous.
 The length in codons is given for each CDS.
 IMPORTANT: This sequence MAY NOT be the entire insert of the
 sequenced clone. It may be shorter because we only sequence a
 overlapping sections once, or longer, because we arrange for a
 small overlap between neighbouring submissions.
 Cosmid c186 is overlapped at the 5' end by cosmid c869, EMBL entry
 SPAC869, accession number AL132779.
 Location/Qualifiers
 1. 30176
 /organism="Schizosaccharomyces pombe"
 /strain="972h-"
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 1. 2929
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 misc_feature
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 2929. 3909
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 pombe., CAB69629, hypothetical serine/threonine repeat
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 TNSVGGASSTACPLFTTYTNGITPGCTTITPTISSTSGVSSNNIDETSVSESIIIT
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 SGTQSGVEVITPCGSPENSHFLKNDKISPSYVMDPNAPRTVINGAGRGNNMFA
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in 319 aa)"
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 AOVCFVNDQVADATLTKALAENGKVLALRCGGYNNVNLKAASEYKIVTVHVPYSXP
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 KCFKMGFGCDVLAIDINPKLENYGVQVFEQNEVLKADFLCHLCLPTFTPTTHVNS
 DSLAMKKGVTTIVTSRGLDITKALVDAIDSGVGGCAIDVVEGSRNLFYKDLSEV
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 10435. 11517
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 transmembrane channel"
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IVTALLAYQVGRASVFPFGSYLALPFMTSPAVLVGRAAPLPFPKSI THILGGTFLIFG
VKMLKESKVESQSLSENEFDKVEKIIIVNEEDMKTLGLPLASNRSSSTLKDFFK
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HMLCTMVAVIVIRTSINKIEMKIVFPGGIVFMIFGLIYIPQGF"
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cerevisiae, YH19, YEAST, hypothetical 32.6 kd protein in
dap2-slt2 intergenic region.hypothetical 32.6 kd protein
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Best Local Similarity 56.4%; Pred. No. 3.9e-66;
Matches 519; Conservative 0; Mismatches 396; Indels 6; Gaps 1;

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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
25060 CTAGTCAATTAATGATGTTGTGTGCTGGAAATGTGGGTCAACTACTCTTTTAC 25001

Qy 102 GTTGCTTCTCAGCGGCATCGTTCCGAGATTGCTTATCGAGTGAACAAAGCAAGC 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
25000 ACTACTACTAAGTGTAGTCTGTAATCGTAACTGTAATCATTTGACTTGAACAAAGCAAGC 24941

Qy 162 AGAGGTGAAGCATGACTTAAACACGAGCAGCACCTTCAAAATACAGGCTCGAG --- 217
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24940 AGAAGGTGAAGCATGACTTAAATCATGAGCTCCACTTTCCATGAGACTCGCGTATA 24881

Qy 218 --CGGGTGATTCTCTGCTGCGTGGCGGCCATGTTATTGTTCACATGTGGATTAA 275
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24880 TTTGGGTGACTATAAAGATTGTAAGGACCGAACGGCAGTGTGTAATTACAGCTGGAAGAA 24821

Qy 276 CCAAAAAATGGACAAACAGGATGGATCTTGTGCAAAAAATGCCAACATTATGCTGGA 335
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24820 TCAAAAGCCAGGTGAACAGAGATGGATCTACTTAAAGCAATATTTCCATCTTTAAGGA 24761

Qy 336 AATCATCCCAATGTTGCCAAATATGCTCCTGTATACCATCTCTGTTATGCCAGATCC 395
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24760 AATCCTTTAGAGAGTCACTAAATATACAAAGATGCCATCTCTTAGTTGCAACCAACC 24701

Qy 396 TGTGATGTTTGGACCTATATTAGCTATAAGGCGTACGGGTTTCCATTAAGCAGATTAT 455
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24700 TGTGATGTTACTTACTTACGCTACATTAAAACTCACAGGATTTCCAGCTCAACGAGTCA 24641
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Qy 516 GATCTCATCGGACGAGCATGATCCCTGTGTAATTTGGAGAACTGGTGATTCGGGTGTC 575
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Qy 576 TGTCTGCTCTTACCAACATCCACGGCATGAAGCTCCGGGATTACTGCGAAAAGCCAA 635
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24520 TGTATGTTCCACGCCAGTATTCGAGACTTTTCACITTCGAGATTTCTGTGAAGAATCTGA 24461

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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24460 GACGAAGTATGATGAACAAGCATTTGAATGAATGCTTTTAAAGAAACAAATAATCCGCTTA 24401

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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24220 TCGCAATTAATTAAGCAAGCTTTCCAAAGACGAGGATGCCAAGCTTGTAGAATCCGTGAA 24161

Qy 936 TCAGATCAATCAGTCAATGA 956
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24160 AGCATCAAGCATGCTATTGA 24140
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RESULT 2

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LOCUS BACLDHAA 1423 bp DNA linear BCT 26-APR-1993
DEFINITION B.megaterium L-lactate dehydrogenase gene.
ACCESSION M22305
VERSION M22305.1 GI:143135
KEYWORDS L-lactate dehydrogenase.
SOURCE B.megaterium (strain DSM 090) DNA, clone pMH/pML.
ORGANISM Bacillus megaterium
REFERENCE 1 (bases 1 to 1423)
AUTHORS Waldvogel,S., Weber,H. and Zuber,H.
TITLE Structure and function of L-lactate dehydrogenases from
thermophilic and mesophilic bacteria. VII. Nucleotide sequence of
the lactate dehydrogenase gene from the mesophilic bacterium
Bacillus megaterium. Preparation and properties of a hybrid lactate
dehydrogenase comprising moieties of the B. megaterium and B.
stearothermophilus enzymes
JOURNAL Biol. Chem. Hoppe-Seyler 368 (10), 1391-1399 (1987)
MEDLINE 98107005
PUBMED 3122782
REFERENCE 2 (bases 1 to 1423)
AUTHORS Suter,F.
JOURNAL Unpublished (1989)
COMMENT [2] revises [1].
Draft entry and computer readable copy of sequence [1] kindly
submitted by S.Waldvogel 02-OCT-1987, and [2] by F.Suter
16-MAY-1989.
Author address [2]
F.Suter
ETH-Hoenggerberg
Inst.f. Molekularbiologie und Biophysik
CH 8093 ZUERICH
Switzerland.
Location/Qualifiers
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FEATURES

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Matches 496; Conservative 0; Mismatches 396; Indels 12; Gaps 3;

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Qy  101  CGTTGCTTCTCAGCGGCATCGTTTCCGAGATTGTCCTTATCGAGCTGAAACAAAGACAAAG 160
Db  329  CAATGGTGAATCAAGGTATTGCCAATGAAATAGTGTATTTCGATATGAAAGAAAG 388

Qy  161  CAGAGGTGAAGCATGGACTTAACACACGACGACCTT-----CAAAATACAAGGTCTC 214
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Qy  215  GAGCGGTGATTATCTCGACTGCGCTGGCGGGCCATTGTTATTGTGCATGTGGGATTA 274
Db  449  GGGCTGGAGATTATAAAGACGTGCTGCACGCTGATTTAGCAGTTATTATACAGCGGCGCTA 508

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Qy  335  AAATCATCCCCAATGTGTGCCAAATATGCTCCTGATACCATCTCTGCTTATTGGCCACGAATC 394
Db  569  GCATTGTAAGAATATTATGAACAGCGGATTTTGACGGCATCAATTTTAGTGGCAACAATC 628

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Qy  455  TCGGCTCAGGTACAGTTCTGGATACTGCTCGTTTTAAATATCATCTCGGAGAGACATTTCA 514
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Qy  515  AGATCTCATCGGACAGCATCGATCGCTGTGTAAATGGAGAACATGGTGAATTCGGGTGTGC 574
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Qy  575  CTGTCTGGTCTTTTACCAACATCGACGGGATGAAGCTCCGGGATTACTGCGAAAAAGCCA 634
Db  809  CTGTTTGGAGCCACGCGCAAAATTGGCGGTGTGAAGCTCGAAACATTTTATCAATACTGCCG 868

Qy  635  ACCACATATTGTATCAGAAATCGGTTCCATAGAAATCTTTTGACAAACCGGAGACGCTGCTT 694
Db  869  CTAATTGAAAAAGAACCGGATATGAGCATCTATTTC---GAACAACCCGGATCGGCTT 925

Qy  695  ACGATATCATCAAGCGCAAAAGGCTTATCTTCATATGGAATCGCAGCGGATTTACTTCGCA 754
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Qy  755  TAGTAAAGCGGATTTTAGAGGATACAGATCCACACTTACAGTTTCAAC---CGTTGGT 811
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RESULT 4			
AE007540			
LOCUS	AE007540	11158 bp	DNA linear BCT 27-JUL-2001
DEFINITION	Clostridium acetobutylicum ATCC824 section 28 of 356 of the complete genome.		
ACCESSION	AE007540	AE001437	

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VERSION AB007540.1 GI:15023104
KEYWORDS
SOURCE
ORGANISM
Clostridium acetobutylicum.
Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
REFERENCE
1 (bases 1 to 11158)
Nolling,J., Bregon,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P.,
Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum
J. Bacteriol. 183 (16), 4823-4838 (2001)
21359325
REFERENCE
11466286
2 (bases 1 to 11158)
Childress,D., Zeng,Q. and Smith,D.R.
Direct Submission
TITLE
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
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BASE COUNT 4051 a 1350 c 2112 g 3645 t
ORIGIN

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Best Local Similarity 53.3%; Pred. No. 2.2e-47;
Matches 475; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

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QY 112 AGCGGCATCGTTTCCGAGATGTTCCTTATCGACGTGAACAAACAGACAGAGGGTAA 171
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197 GGTGGACTTGCATCTGAGATAGTTATAGTAGATGTAATAAGATAGGCAAGAGGGAA 256
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REFERENCE 2 (bases 1 to 301450)
AUTHORS Shimizu,T.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2001) Tohru Shimizu, Institute of Basic Medical
Sciences, University of Tsukuba, Department of Microbiology, 1-1-1
Tennohdai, Tsukuba, Ibaraki 305-8575, Japan
(E-mail: tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,
Fax:81-298-53-3354)
Location/Qualifiers
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(446 aa); 60.7% identity in 448 aa overlap
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Query Match 19.1%; Score 185.8; DB 1; Length 301450;
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QY 43 AAAACAGTAAAGTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCACAGCGTATACG 102
 DB 142778 AAAACTAATAAACTCAATAATAGTGCAGATTTGTGTTCACACAGCTTCGCA 142719
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 DB 142718 TTAATGCAAGATGATTAGCATCCGAAATAGTAATTTGTGATATAAATAGGATAAGCA 142659
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QY 517 ATCTCATCGGACAGCATCGATCGCTGTGTAAATTTGGAGACATCGTGTATTCGGGTGCGCT 576
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RESULT 7
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 DEFINITION Sequence 1411 from Patent WO0134809.
 ACCESSION AX142689
 VERSION AX142689.1 GI:14282216
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS Kimmerly, W.J.
 TITLE Staphylococcus epidermidis nucleic acids and proteins
 JOURNAL Patent: WO 0134809-A 1411 17-MAY-2001;
 GLAXO GROUP LIMITED (GB)
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 BASE COUNT 339 a 130 c 194 g 306 t
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Query Match 18.9%; Score 183.8; DB 6; Length 969;
 Best Local Similarity 53.0%; Pred. No. 2.1e-42;
 Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;

QY 51 AAAAGTTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGCGTATACGTTGCTTCT 110
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 QY 111 CAGCGGCATGTTTCCGAGATTCTCTTATCGACGTGMAACAAAGACAAAGCAGAGGTGA 170
 DB 96 TCAAGAAATTCAGATGAATTTGTAATTTATGATTTGCAAAAGATAAGTGAAGCAGA 155
 QY 171 AAGCATGGACTTAAACACGACGACCTTTCAATAACAAGGTCTCG-----AGCGG 221
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QY 282 AATGGACAAACAAAGGATGGATCTTGTGCAAAAAATGCCAAACATTAATGCTGGAATCAT 341
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 DEFINITION Sequence 2383 from Patent WO0134809.
 ACCESSION AX143661
 VERSION AX143661.1 GI:14282702

KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS Kimmerly, W.J.
 TITLE Staphylococcus epidermidis nucleic acids and proteins
 JOURNAL Patent: WO 0134809-A 2383 17-MAY-2001;
 GLAXO GROUP LIMITED (GB)

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RESULT 9
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 VERSION AF270315.1 GI:9624227
 KEYWORDS
 SOURCE Staphylococcus epidermidis.
 ORGANISM Staphylococcus epidermidis.
 REFERENCE 1 (bases 1 to 3019)
 AUTHORS Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M.,

Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listerbee, S., Ashanti, C., Altschuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
TITLE Transposon-mediated sequencing of the *Staphylococcus epidermidis*
genome
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 3019)
Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listerbee, S., Ashanti, C., Altschuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3398, USA
LOCATION/Qualifiers
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Best Local Similarity 53.0%; Pred. No. 2.3e-42;
Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;
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DB 1492 AACTAGTGTATGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 1433
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LOCUS AX145633 3019 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 4355 from Patent WO0134809.
ACCESSION AX145633
VERSION AX145633.1 GI:14284198
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 3019)
AUTHORS Kimmerly, W.J.
TITLE *Staphylococcus epidermidis* nucleic acids and proteins
JOURNAL Patent: WO 0134809-A 4355 17-MAY-2001;
GLAXO GROUP LIMITED (GB)
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Best Local Similarity 53.0%; Pred. No. 2.3e-42;
Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;
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DEFINITION	Staphylococcus epidermidis strain SRI clone step.1022a07 genomic sequence.
ACCESSION	AF269753
VERSION	AF269753.1 GI:9633650

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Staphylococcus epidermidis.
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 4093)
Kimmerly, W. J., Taylor, J. David., Neisen, A. J., Godlevski, M. M.,
Rubino, M. A., Nelson, F. J., Rivers, P. R., Torruella-Miller, I.,
Listenes, S., Ashanti, C., Altschuller, G., Mamo, L., Shepherd, N. S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D. H., Miller, G. S. and
Furdon, P. J.

TITLE	JOURNAL	REFERENCE	AUTHORS
Transposon-mediated sequencing of the <i>Staphylococcus epidermidis</i> genome	Unpublished	2 (bases 1 to 4093)	Taylor, J. David., Kimmerly, W.J., Neilsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.C., Rivers, P.R., Tortuella-Miller, I., Listennee, S., Ashanti, C., Altshuller, G., Mam, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and Furdon, P.J.
TITLE	JOURNAL	REFERENCE	AUTHORS
Submitted (22-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore Drive, Research Triangle Park, North Carolina 27709-3398, USA			
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DEFINITION	Sequence 3793 from Patent WO0134809.
ACCESSION	AX145071
VERSION	AX145071.1
KEYWORDS	GI:14283636
ORGANISM	synthetic construct.
SOURCE	synthetic construct.
linear	PAT 31-MAY-2001

Query Match 18.9%; Score 183.8; DB 1; Length 4093;

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LOCUS TMLDH 1130 bp DNA linear BCT 05-OCT-1993
DEFINITION T.maritima ldh gene.
ACCESSION X74302
VERSION X74302.1 GI:396280
KEYWORDS lactate dehydrogenase; ldh gene.
SOURCE Thermotoga maritima.
ORGANISM Thermotoga maritima
Bacteria; Thermotogae; Thermotogae; Thermotogales; Thermotogaceae;
Thermotoga.
1 (bases 1 to 1130)
Ostendorp,R.
Direct Submission
TITLE Submitted (23-JUL-1993) R. Ostendorp, Universitaet Regensburg, Inst
fuer Biophysik & Physikal Biochemie, Universitaetsstr. 31, 93053
Regensburg, FRG
2 (bases 101 to 1075)
Ostendorp,R., Liebi,W., Schurig,H. and Jaenicke,R.
TITLE The L-lactate dehydrogenase gene of the hyperthermophilic bacterium
Thermotoga maritima cloned by complementation in Escherichia coli
Eur. J. Biochem. 216 (3), 709-715 (1993)
JOURNAL 94009031
MEDLINE 8404889
PUBMED

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-10_signal

RBS

gene

CDS

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BASE COUNT 340 a 238 c 291 g 261 t
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AE001823

LOCUS

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AE001823 AE000512
ACCESSION AE001823.1 GI:4982441
KEYWORDS
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ORGANISM Thermotoga maritima.
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae;
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1 (bases 1 to 12762)
Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J.,
Hart, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A.,
McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M.,
Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A.,
Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D.,
Eisen, J.A., Fraser, C.M. et al.
Evidence for lateral gene transfer between Archaea and bacteria
from genome sequence of Thermotoga maritima
Nature 399 (6734), 323-329 (1999)
99287316
PUBMED 10360571
REFERENCE
AUTHORS 2 (bases 1 to 12762)
Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J.,
Hart, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A.,
McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M.,
Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A.,
Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D.,
White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
Direct Submission
Submitted (01-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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Query Match      18.2%; Score 176.6; DB 1; Length 12762;
Best local Similarity 52.3%; Pred. No. 3; Se-40;
Matches 467; Conservative 0; Mismatches 414; Indels 12; Gaps 3;

QY 50 TAAAGTTGTGGTAGTGGAGTGGAGTGTGGGTCTGCCACAGCGGTATACGTTGCTTC 109
DB 8603 TGAANAATAGGTATCGTAGGACTCGGAAGGGTGTGGTTCAGACACGGCTTTGCACTCCTCGA 8662

QY 110 TCAGCGGCATCGTTCCGAGATTGTCCTTTATCGACGTGAACAAAGACAAAGCAGAGGGTG 169
DB 8663 TGAAGGTTTTCGAGGGAATGGTTCTGTATAGACGTGCGNTAAGAAAGAGCAGAGGAG 8722

QY 170 AAAGCATGCACTTAACACGACGACGACCTTCAAAATCAAGGTC-----TCGAGCGGGTG 223
DB 8723 ACGCTCTCGATCTCATTCACGGAACACCTTTCACGAGAAGAGCGAACATCTACGCTGGAG 8782

QY 224 ATTATCCTGACTCGCGTGGCGGCCCATGTTATTGTTCATGTCATGTGGATTACCAAAAAA 283
DB 8783 ACTATCGGATCTGAAAGGATCAGATGTGGTGTGATCGTCTCGGGGAGTACCTCAGAAAC 8842

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Search completed: July 31, 2003, 09:42:47
Job time : 2773 secs

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QY 284 ATGGCAAAACAAGGATGGATCTTGCTGCAAAAAATGCCAACATTATGCTGGAAATCATCC 343
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QY 344 CCAATGTTCCAAAATATGCTCTGTATACCATCTGCTTATTGCGACGAATCCTGTGATG 403
DB 8903 GAAACGCTCTCCAAATACGCTCTGTATTCGATTGTGTCATCGTGGTTCACGAATCCCGTGCATG 8962

QY 404 TTTTGACCTATATTAGCTATAAGGCGTCAGGGTTTCCACTAAGCAGATTCCTGGCTCAG 463
DB 8963 TCTCAGCTATTCTTCTCTCAAGAGTCCGGAATGGATCCCAAGAAAGGTGTTCCGGTCCG 9022

QY 464 GTACAGTCTCGGATCTGCTGCTTTTAAATACATCTCGGAGAGCACTTCAAGATCTCAT 523
DB 9023 GAACGGTCTCGACACAGCAAGCGCTCAGAACTTTGNTAGCGCAACTGGGGCTTTTCTC 9082

QY 524 CGGACAGCATTCGATGCTGTGTAATTGGAGAACATGTTGCGGTGTCCTGTCTGCTG 583
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QY 584 CTCCTTACCAACATCGACGCGCATGAGCTCCGGGATTACTGCGAAAAAGCAACCATAT 643
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QY 644 TTGATCAGAAATCGGTTTCCATAGAACTCTTTGAGCAAAACGGGAGACGCTGTACGATATCA 703
DB 9200 GCGATTTCGAAGATCTGGAATACTTCGCTGAAAAAACCAAAAGAGCGGTACGAGATCA 9259

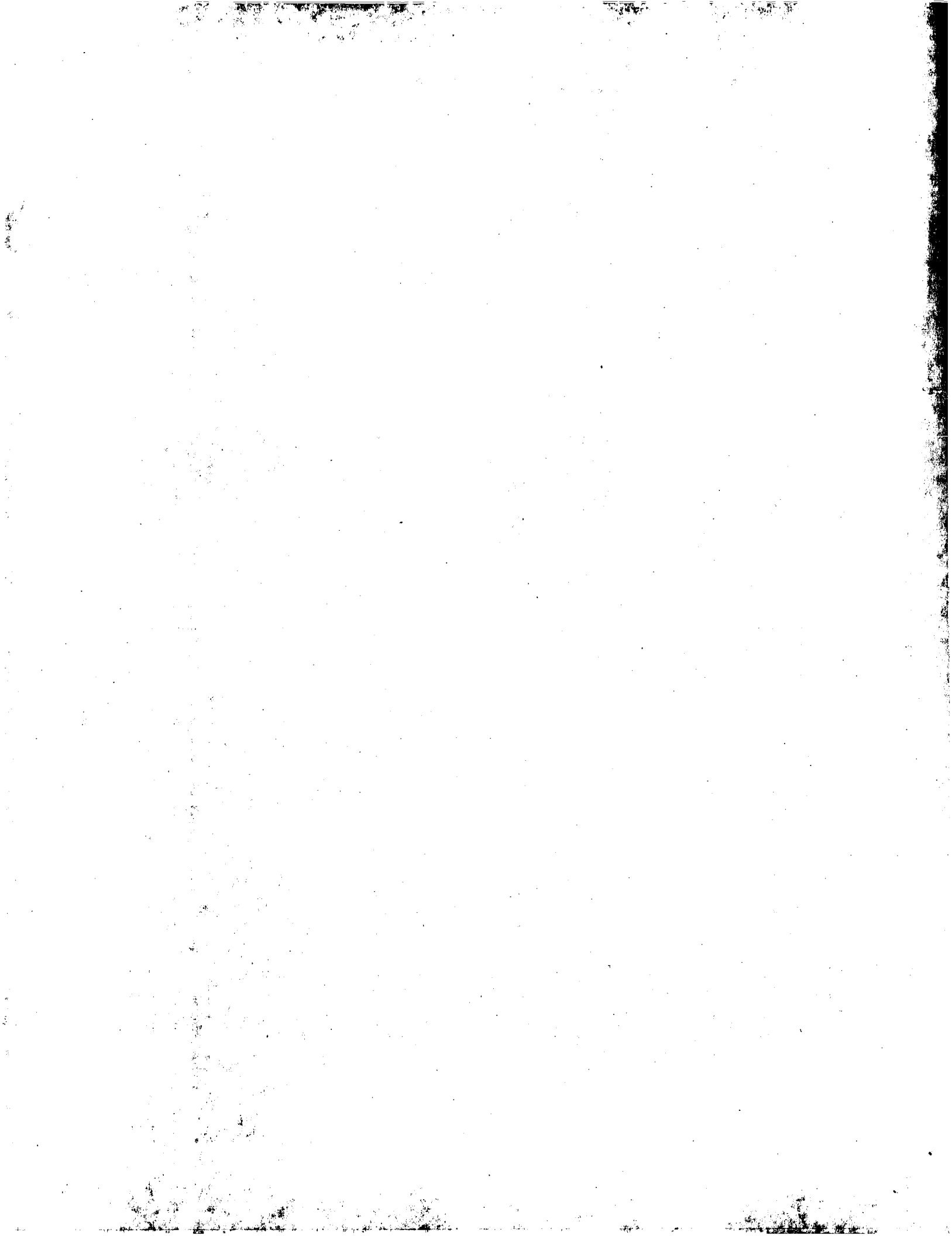
QY 704 TCAAGCGCAAGGCTATCTTCAATATGGAATCGCAGCGGGATTACTTCCATAGTAAAGG 763
DB 9260 TAGAGAGAAAGGAGCCACCCATTACGCCATAGCTCTCGCCGTGGCCGACATAGTGGAGA 9319

QY 764 CGATTTTAGAGATACAGGATCCACACTTACAGTTTCAACCGTT---GGTGATTATTTG 820
DB 9320 GCATCTTCTTCGACGAAAGAGAGTGCTTTACGCTTTTTCGTTATCTCGAAGATTACCTCG 9379

QY 821 GGGTTTGAACAAATTCGTATAAGCGTCCCTTACCAACTCAATAAAGTGGGGCTCATCAAG 880
DB 9380 GTGTAAGATCTCTGTATCAGTGTCTCTGTTTACCTTGGAAAGCAGCGAGTGGAAAGAA 9439

QY 881 TGGCTGAATTTCACTCGGATGAGAGGAATAAGATTGATGAAAAAATCAGCT 933
DB 9440 TCCTCGAACTGAACCTCGAACGAAGAAGAACTGGAAGCCTTTCAGAAAGTCAGCT 9492

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 06:50:56 ; Search time 278 Seconds
(without alignments)
7873.893 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
C 1	205.2	21.1	2365589	24 ABA90521	Genomic sequence o
2	186.2	19.2	28690	20 AAX13075	Enterococcus faeca
3	183.8	18.9	969	22 AAH53009	S. epidermidis ope
4	183.8	18.9	969	22 AAH53495	S. epidermidis ope
5	183.8	18.9	993	24 ABA92028	Staphylococcus epi
6	183.8	18.9	3019	22 AAH54991	S. epidermidis gen
7	183.8	18.9	4093	22 AAH54429	S. epidermidis gen
8	183.6	18.9	1255	24 AAD37417	Bacillus strain LN
9	173	17.8	13154	20 AAX13275	Enterococcus faeca

10	172.6	17.8	3264	18 AAV74735	Staphylococcus aur
11	157.2	16.2	981	24 ABA68374	Streptococcus poly
12	155.8	16.0	945	20 AAZ09139	B. flavum lactate
13	155.8	16.0	1065	22 AAF71424	Corynebacterium gl
14	154.2	15.9	942	22 AAF68175	C glutamicum codin
15	154.2	15.9	309400	22 AAH68534	C glutamicum codin
C 16	154.2	15.9	1163020	24 ABQ67197	Listeria innocua c
C 17	154.2	15.9	3011208	24 ABQ69245	Listeria innocua c
C 18	153.6	15.8	5278	19 AAV52360	Streptococcus pneu
C 19	153.4	15.8	2944528	24 ABA03041	Listeria monocytog
20	151	15.5	747	24 ABK72782	Bacillus lichenifo
21	149	15.3	1197	12 AAG10162	L-lactic acid dehy
22	147.2	15.1	5449	21 AAC64598	Streptococcus pneu
C 23	146.2	15.0	14280	18 AAV74368	Staphylococcus aur
C 24	142.6	14.7	3073	12 AAQ15280	L-lactic acid dehy
25	138.8	14.3	1234	9 AAN80494	Sequence encoding
26	136	14.0	1680	24 AAS17494	Human cDNA encodin
27	136	14.0	1759	22 AAH64738	Human secreted pro
28	133.4	13.7	910715	20 AAX20248	Borrelia burgdorfe
29	132.8	13.7	987	24 ABA68373	Streptococcus poly
C 30	132.8	13.7	2155561	24 ABA71527	Streptococcus poly
C 31	129.2	13.3	2621	24 ABQ70916	Listeria monocytog
32	128.4	13.2	1856	20 AAX97742	Extended human sec
33	125	12.9	1661	21 AAG09330	Human cancer assoc
34	125	12.9	1661	24 ABK84497	Human cDNA differe
35	125	12.9	1732	22 AAI59428	Human polynucleoti
36	125	12.9	1792	22 AAI61214	Human polynucleoti
37	125	12.9	2223	22 AAH72820	Human cervical can
38	125	12.9	2224	22 AAH72872	Human cervical can
39	123.6	12.7	1261	21 AAC42568	Arabidopsis thalia
40	121.8	12.5	950	20 AAX61751	B. burgdorferi ant
41	121.2	12.5	4913	24 AAD37416	Bacillus strain TN
42	120.8	12.4	1755	22 AAH64739	Human secreted pro
43	118.8	12.2	1519	24 ABQ69016	Listeria monocytog
44	116.6	12.0	29559	23 AAS59546	Propionibacterium
45	115.8	11.9	887	20 AAX61752	B. burgdorferi ant

ALIGNMENTS

RESULT 1
ABA90521/c
ID ABA90521 standard; DNA; 2365589 BP.

XX ABA90521;

XX AC

DT 16-MAY-2002 (first entry)

XX Genomic sequence of Lactococcus lactis IL1403.

XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.

XX Lactococcus lactis IL1403.

XX FR2807446-A1.

PD 12-OCT-2001.

XX 11-APR-2000; 2000FR-0004630.

XX 11-APR-2000; 2000FR-0004630.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX WPI; 2002-043418/06.

XX New nucleotide sequence useful in the identification or Lactococcus

XX lactic and related species -

XX Claim 1; SEQ ID 1; 2504pp; French.

XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (AB90521) and related proteins (ABBS3300-ABBS5621). The
CC nucleic acid sequence is useful in the detection and/or amplification of
CC nucleic acid sequence, particularly to identify Lactococcus lactis or
CC related species. The proteins of the invention are useful for the
CC biosynthesis or biodegradation of a composition of interest. The
CC invention helps research in lactic bacteria, particularly useful in the
CC production of yogurt and cheese.
CC Note: The sequence data for this patent is based on equivalent patent
CC WO2001/77334 (published 18-Oct-2001) which is available in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
Query Match 21.1%; Score 205.2; DB 24; Length 2365589;
Best Local Similarity 53.4%; Pred. No. 1.6e-52;
Matches 507; Conservative 0; Mismatches 428; Indels 15; Gaps 3;
QY 29 TAAGAACTGATGCCAAACACAGTAAAGTTGGTAGTGGGAGTGGGAGTGGGCTG 88
DB 380506 TAAAAATGAAATTAACAGCGAAGAGTAGTTTATAGAACAGGTTTGTGGAAACAA 380547
QY 89 CCACAGCGTATACGTTGCTTCTCAGCGGCATCGTTTCCGAGATTGCTTTATCGACGTGA 148
DB 380546 GTATTGCTTATCAATGATTAAATCAAGGACTTGTTAATGAGTTGGTTTATAGATGTTA 380487
QY 149 ACAAGACAAAGCAGAGGGTGAAGCATGGACTTAAACACGACGACCTTC----- 200
DB 380486 ATCAGGATAAAGCTGAGGGTGAAGCCTTAGATTATTATAGATGGGCTTTCTGGGGCAAG 380427
QY 201 -AATACAGGCTCGAGCGGTGATTATCTGACTCGCTGGCGCGCCATTGTTATTG 259
DB 380426 AAAATGTTATGTCAGAGCTGGAGATTATAGGATTGTAAGACGCTGATATTGTGCTG 380367
QY 260 TCACATGTGGGATTAAACCAAAAAATGACAAACAGGATGGATCTTCTGCGCAAAAAATG 319
DB 380366 TTACGGCTGGGGTAAATCAAAACACAGTCAATCACTGTTAGATTGTTTAAATACAAATG 380307
QY 320 CCAACATATGCTGGAATCATCCCAATGTTGCCAATATGCTCTGATACCATCTGCG 379
DB 380306 CTAAAAATTATGCTGCTCAATCGTACTCAGGTTATGGACTCAGGTTTGTGGTATTTTG 380247
QY 380 TTATTGCCACCAATCTGTCATGTTTGAAGTATATAGCTATAGGCGTCAAGGCTTC 439
DB 380246 TAATTGCTTCAATCTGTGGAATTTTACCTAATGCTGCTTGGGAACCTTCTGCTTG 380187
QY 440 CACTAAGCAGAGTTATCGGCTCAGGTACAGTTCTGGATACGTTCTGTTTAAATACATCC 499
DB 380186 ATCAATCTCGAATTTGCGAACTGCTACAACTTTGGATACCTACTCTGTTTAAAGAAAT 380127
QY 500 TCGGAGAGCATTCAAGATCTCATCGGACAGCATCGATGCTGTGTAATTGGAGAAATG 559
DB 380126 TGGCCACAAAGCTAGAAATTTGATCCAGGAGCGTTTCATGATATATATTATTTGGCAACATG 380067
QY 560 GTGATTGGGTTGCTGCTGCTGCTCTTACCAACATCGAGGATCAAGCTCGGGAATT 619
DB 380066 CGGATTCGAAGTTGGAGTTTGGTTCACACGACGGTAGTGGAAACCTTATCTTGAAT 380007
QY 620 ACTCGAAAAAGCCACCAATATTTGATCAGAAATGGTTTCCATAGAAATCTTTGAGCAAA 679
DB 380006 TTATTGTTAAAAATAAAAAATAGGGTTGAAGATTGTTCTAAATTTGCAATAAGGTAA 379947
QY 680 CGGAGAGCGTCTTACGATATCATCAAGCGCAAGGCTATACCTTATATGGAATCCAG 739
DB 379946 ---AAAAATGCTGCTATGAGATTATGTAATAAAACAGGCTACTTATTACGGCAATTGAA 379890
QY 740 CGGATTAATCTCGCATAGTAAGCGGATTTTAGAGGATACAGGATCCACACTTACAGTTT 799
DB 379889 TGAGTACAGCTAGAAATGTCAGGCCCATCTTAATATATACAGCAATCTTACCAGTTT 379830
QY 800 CAACC---GTTGGTGAATTTTGGGGTTGAACAAATTTGCTATAGCGCTCCCTACCAAC 856

DB 379829 CTGCCTATTATTTACGTGGTGAATATGGTCAAGAGGTGCTTTTACCGGTGTTCCATCTATTG 379770
QY 857 TCATATAAAGTGGGCTCATCAAGTGGCTGAACCTTTCACTCGATGAGAGGAATAGAAT 916
DB 379769 TAAATCAAAATGGTGTGTAGAGAAATCATTTGAATTAATATTGATGCTTATGAAAGAAAC 379710
QY 917 TGATGAAAAAATCAGCTAGTCTAGATCAAAATCAGTGAATGAGCATCTGAG 966
DB 379709 AATTGAAAAATCTGTCACTCACTTAAGAGAGGTAAAGATTAATCTATTAG 379660
RESULT 2
AA13075
ID AA13075 standard; DNA; 28690 BP.
XX AC AA13075;
XX DT 19-MAR-1999 (first entry)
XX DE Enterococcus faecalis genome contig SEQ ID NO:138.
XX KW Enterococcus faecalis; contig; detection; Enterococcal infection;
XX KW vaccine; attenuation; computer readable medium; ds.
XX OS Enterococcus faecalis.
XX PN WO980555-A2.
XX PD 12-NOV-1998.
XX PF 04-MAY-1998; 98WO-US08985.
XX PR 14-NOV-1997; 97US-0066009.
XX PR 06-MAY-1997; 97US-0044031.
XX PR 16-MAY-1997; 97US-0046655.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Barash SC, Dillon PJ, Kunsch CA;
XX WPI; 1999-045171/04.
XX New isolated Enterococcus faecalis polynucleotides and polypeptides
- used to develop products for the detection of Enterococcus and for
use in vaccines for prevention or attenuation of Enterococcus
infection.
PS Claim 1; Page 816-830; 2084pp; English.
XX A computer readable medium has been developed which has recorded on it
982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC AA12938 to AA13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.
XX Sequence 28690 BP; 8977 A; 5769 C; 4894 G; 9006 T; 44 other;
Query Match 19.2%; Score 186.2; DB 20; Length 28690;
Best Local Similarity 52.5%; Pred. No. 1.6e-47;
Matches 481; Conservative 1; Mismatches 420; Indels 14; Gaps 3;
QY 51 AAGATTGTTAGTGGAGTGGAGTGGTGGTTCGCCACGAGCTATACGTTGCTTCT 110
DB 16610 AAAAGTCGAATTTATTTGGTACTGTTTGTGGCAAGATTGCTTATTCATGATCAA 16669

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QY 111 CAGCGGCATCGTTCCGAGATGTCTTATCGAGTGAACAAAGACAAAGACAGAGGCTGA 170
Db 16670 CCAAGGATTCGGAATGAATTAATCTTAGTTGATTTGACAAAGCCAAATCTGAGCGGA 16729
QY 171 AAGCATGGACTTAACACAG-----CAGCACCCTTCAAAATCAAGGTCTCGAGCGGT 222
Db 16730 NCAATTGACTTATTAGATGTGTGKCYTGGGKCMAGAAAATGTAAACGCTCGGGCTGGC 16789
QY 223 GATTATCCTGACTGCTGCGCGGCCATTTGTTATGTCACATGTGGGATTAACCAAAA 282
Db 16790 GACTATCAAGACTGCCAAGATCGGATATCGTGTGATTAACGCTGGCGTATCAAAA 16849
QY 283 AATGGACAAACAAAGATGGATCTTGTCTGCAAAAATGCCAACATTAATGCTGGAAATCATC 342
Db 16850 CCTGGGCAAGTCTGTAGATTTGGTTTCAATCAATGCAGAAATTAATGAACAATGTT 16909
QY 343 CCAATGTTGCCAAATATGCTCTGATACCATCTGTTATTCGACAGGAATCTGTGCGAT 402
Db 16910 AACAATATCAAGAAATCTGTTTGTGATGGAATTTAGTGAATTTAGCTCAAAATCTGTGAT 16969
QY 403 GTTTTGACCTATATAGCTATAGGCGTCAAGGCTTCCACTAAGCAGAGTTATCGGCTCA 462
Db 16970 GTACTGACTTATGGCTCGCAGCTTCGGTTTACCTGTTTCAAGAGTAATGGAAT 17029
QY 463 GGTCAGTCTGATCTGCTCGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCA 522
Db 17030 GGTACAACTTTGGACAACTCGTTTCCGCAAAAGACTGCTCAACGTTTAGCGATTGAT 17089
QY 523 TCGGACAGATCATGCTGTGTAATGGAAGACATGTTGATTCGGGTGTCCTGTCTGG 582
Db 17090 CCAAGCAATGTTCAAGCTATATTTTGGGCAACAGCGGATTTCTGAAGTGGCTGTCTGG 17149
QY 583 TCTCTTACCAACATCGAGCGCATGAGCTCCGGGATTTACTGCGAAAGCCACACATA 642
Db 17150 TCTCATACCATGATGTGTACCAACCTATTTTGAATTTGTGATACGACAGAGCGCTTA 17209
QY 643 TTTGATCAGATCGTTTCCATAGAACTTTGAGCAAAACGCGAGCGCTGTCTACGATATC 702
Db 17210 ACTAGTGACGAT--TTACCAATCAITTTCTGATATAAGTGAANAATACAGCTTATGAAT 17266
QY 703 ATCAAGGCAAGAGCTATCTTATATGAAATCGCAGCGGATTAATCTGCAATAGTAAAG 762
Db 17267 ATCGATCGCAACAAAGCGACTTATTTAGGATTTGGTATGATGACTGTCAGCGCATTTGTA 17326
QY 763 GCGATTTAGAGGATCAGATCCACACTTACAGTTTCAAC---CGTGTGTATTTT 819
Db 17327 GCGATTTTAAATATGAACAGCTATTTTACCTGTCTCAGCTTACTTAGATGGCAATAT 17386
QY 820 GGGGTTGAACAAATTCGTATAGCGTCCCTACCAAACTCAATAAAAGTGGGCTCATCAA 879
Db 17387 GGGCAACAAAGATGTATTTACAGGATTCCTGCACTCGTTGGCAATCAAGGTGTGACTGAC 17446
QY 880 GTGGCTGAATCTTCACTCGATGAGAGGAATAGATGATGAAATAATCAGCTAGTCTAG 939
Db 17447 ATTATTGAATGAAATCTGAAATCGCGTGAAGAAAGACTCTTCCAAAATAATCAGTGACAA 17506
QY 940 ATCAAAATCAGTGATTG 955
Db 17507 TTAACACAGTGATGG 17522
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RESULT 3

AAH53009

ID AAH53009 standard; DNA; 969 BP.

XX AC

AAH53009;

XX 03-SEP-2001 (first entry)

XX DT

XX S. epidermidis open reading frame nucleotide sequence SEQ ID NO:1411.

DE DE

XX Staphylococcus epidermidis SRI strain; infection; diagnosis;

KW

vacination; endocarditis; ds.
Staphylococcus epidermidis.
W0200134809-A2.
17-MAY-2001.
09-NOV-2000; 2000WO-US30782.
09-NOV-1999; 99US-0164258.
(GLAX) GLAXO GROUP LTD.
Kimmerly WJ;
WPI; 2001-316495/33.
P-PSDB; AAG82159.
Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
useful for vaccinating against infections, e.g. endocarditis -
Claim 8; Page 398-399; 2188pp; English.
AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
(I) and (II) can have antibacterial activity and therefore can be used
in vaccination. The nucleic acids (I) may be used to produce the
S. epidermidis polypeptides (II) via the production of vectors
containing them which are used to produce hosts cells which express the
polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
used to vaccinate subjects and to raise antibodies against the bacteria.
The polypeptides may also be used to assay for other inhibitors of their
activity and therefore identify compounds that may be used for the
treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
AAH55090 represent specifically claimed S. epidermidis genomic DNA
polynucleotide sequences from the present invention. AAH55091 to
AAH55098 represent oligonucleotide sequences and primers which are used
in the exemplification of the present invention.
N.B. The present invention specifically claims all the polynucleotide
sequences given in the sequence listing of the present specification,
however the sequence listing only goes up to SEQ ID NO:4454 so even
though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
no sequences are present for SEQ ID NO:4455 to 4464.
Sequence 969 BP; 339 A; 130 C; 194 G; 306 T; 0 other;

Query Match 18.9%; Score 183.8; DB 22; Length 969;

Best Local Similarity 53.0%; Pred. No. 1.5e-47;

Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;

QY	51	AAAGTTGTTGGTAGTGGAGTGGGAAGTGTGGTCTGCCACAGCGTATACGTTGCTTCT	110
Db	36	AAAGTTGTTGGTAGTGGAGTGGGAAGTGTGGTCTGCCACAGCGTATACGTTGCTTCT	95
QY	111	CAGCGGCATCGTTTCCGAGATTTGCTTATCGAGTGAACAAAGACAAAGACAGAGGCTGA	170
Db	96	TCAGGAATTCAGATGAATTTGTAATTTATGATATTCGAAAGATAAGTGAAGCAGA	155
QY	171	AAGCATGGACTTAAACCGACGACACCTTCAAAATCAAGGTCTCG-----AGCGGG	221
Db	156	CGTTAAAGATTTAAACCATGGTGCACTTTACAGTTCTTCCACGAGTCACTGTAAGCTGG	215
QY	222	TGATTTATCTGACTGGCTGGCGGCCATTTGTTATTTGTCACATGTGGGATTAACCAAAA	281
Db	216	AGAATATGAAGATTGTAAGATGCAGATTTAGTTGTTATTACAGCAGGTGCACTCAAAA	275
QY	282	AAATGGACAAACAGGATGATCTTGTCTGCAAAAATGCAACATTTATCTGGAATCAT	341
Db	276	ACCGGTGAACTCGTTTACACTTTGTGAGAAAATACTAAATCATGAAAGTATCGT	335
QY	342	CCCAATGTGCAAAATATGCTCTGTATACCATCTGCTTATTTGCGACGAATCTCTGTGCA	401

336 AACTAGTGTGATGATAGTGGCTTTGATGTTCTTCTTAATTCCTGCAACACCGATTGA 395
 402 TGTGTTGACCTATATAGCTATTAAGCGGTGAGGTTTCCACTAAGCAGAGTTATCGGCTC 461
 396 TATCTTAACACGTTATGTTAAAGAAAGTTACAGGTTTACCAGCTGCAAGCTGTTATGCTTC 455
 462 AGGTACAGTGTGATGATCTGCTGTTTAAATTCATCATCTCGGAGAGCACTTCAAGATCTC 521
 456 TGGTACAGTGTGATGATGCAAGATTCAGATATTTAATTAAGTAAGAAATAGGTGTAC 515
 522 ATCGGACAGCATCGATCGCTGTGTAATTTGGAGAACATGTTGCGGTGTGCTGTCTG 581
 516 ATCAAGTAGTGTTCACGCTAGCATTTATAGGTGAACATGGTGTGACTCTGAACTTGCAGTTG 575
 582 GTCTCTTACCAACATCGACGCGCATGAAGCTCCGGGATTAATCTGCGAATAACCAACACAT 641
 576 GTCTCAAGCAACGTTGGAGGATTTTCAGTGTATGATACATTTGAAGAAGAAACTGGTAG 635
 642 ATTTGATCAGAATCGGTTCCATAGAAATCTTTGAGCAACGCGAGACGCTGCTTACGATAT 701
 636 CGATGCTAA-----ACGGAATGAATTTATTAATACAGAGATGCTGCTTACGATAT 689
 702 CATCAAGCGCAAGGCTATATCTCATATGGAATCGCAGCGGGATTAATTCGCATAGTAA 761
 690 CATTCAGCTAAAGGATCTAGTATTTATGTTAGTCTTAGCACTATTACGTTATTTCTAA 749
 762 GGCATTTTACAGATACAGATCCACACTTACAGTTTCAA---CCGTTGGTGAATATTT 818
 750 AGCTTTTACTAAATTAAGAAATAGTATTTTGACAGTTTCTAGTCAACTTAATGGTCAATA 809
 819 TGGGGTTGACAAATTCGTATAAGCGTCCCTTACCATACTCAATAAAGTGGGCTCATCA 878
 810 TGGATTTAACAGATTTATCTTGCTTACCACACTTATCAATCAATATGTCAGTTAA 869
 879 AGTGGCTCAACTTTCACTCGATGAGAGGAATAGAAATTTGATGAAAAAATCAG 931
 870 AATTATGAACACCATTAATATGATACGAACACTACAATTTACTAGAAAAATCAG 922

RESULT 4

AAH53495
 ID AAH53495 standard; DNA; 969 BP.
 AC AAH53495;
 XX
 XX 03-SEP-2001 (first entry)
 DT
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2383.
 DE
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW Staphylococcus epidermidis;
 KW Staphylococcus epidermidis;
 OS
 XX
 XX WO200134809-A2.
 XX
 XX
 XX 17-MAY-2001.
 XX
 XX 09-NOV-2000; 2000WO-US30782.
 XX
 XX 09-NOV-1999; 99US-0164258.
 XX
 XX (GLAXO) GLAXO GROUP LTD.
 XX
 XX Kimmerly WJ;
 XX
 XX WPI; 2001-316495/33.
 DR P-PSDB; AAG82645.
 XX
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 XX
 XX Claim 8; Page 629-630; 2189pp; English.

XX
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though the sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 969 BP; 339 A; 130 C; 194 G; 306 T; 0 other;
 Query Match 18.9%; Score 183.8; DB 22; Length 969;
 Best Local Similarity 53.0%; Pred. No. 1.5e-47;
 Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;
 QY 51 AAAAGTTGGTAGTGGGAGTGGGAAGTGTGGGTTCGCCACAGCGTATACGTTGTTCT 110
 DB 36 AAAAGTTGTTTAGTAGGAGACGGTTCGCTAGTTCAGTTATGCTATGCTATGCTGAC 95
 QY 111 CAGCGCATCGTTTCCGAGATTCCTTATCAGCTGAACAGACAGACAGAGCGGTGA 170
 DB 96 TCAAGGAATTCAGATGAATTTGTAATTAATGATATTGCAAAAGATAAAGTGAAGCAGA 155
 QY 171 AAGCATGGAATTAACACCGCAGACCTTCAATAACAAGTCTCG-----ACGGG 221
 DB 156 CGTTAAAGATTTAACCATGGTGCATTTACAGTTCTTCCACGAGTGTAAAGCTG 215
 QY 222 TGAATATCTGATGCGCTGGCGGCCCATTTGTTATTTGTCACATGTTGGGATTAACCAAA 281
 DB 216 AGAATATGAAGATTGTAAGATGTCAGATTTAGTTGTTATTACAGCAGGTGCACCTCAA 275
 QY 282 AATGCAACAACAAGATGGATCTCTGCAAAAATATGCAAAATATGCTGGAATCAT 341
 DB 276 ACCGGTGAATCTGTTTACAACTTGTGAGAAAAATATCAAAATCATGAAGATATCGT 335
 QY 342 CCCCAATGTTGCCAAATATGCTCTGATACCATCTCTGTTTATTCACCAATCTCTGCGA 401
 DB 336 AACTAGTGTGATGATAGTGGCTTTGATGTTTCTTCTTAATTTGTCGAACCCAGTTGA 395
 QY 402 TGTGTTGACCTATATTAAGCTGTAAGCGGTGACAGGTTTCCACTAAGCAGAGTTATCGGCTC 461
 DB 396 TATCTTTAACACGTTATGTTAAAGAGTTACAGGTTTACCAGCTGGAACGTTTATGCTTC 455
 QY 462 AGGTACAGTCTGATGATCTGCTGTTTAAATATACATCTCCGAGAGCACTTCAAGATCTC 521
 DB 456 TGGTACAGTGTGATGATGCAAGATTCAGATATTTAATTAAGTAAGAAATAGGTGTAC 515
 QY 522 ATCGGACAGCATCGATCGCTGTGTAATTTGGAGAACATGTTGATTCGGGTGTGCTGTCTG 581
 DB 516 ATCAAGTAGTGTTCACGCTAGCATTTATAGTGAACATGGTGTGACTCTGAACTTGCAGTTG 575
 QY 582 GTCTCTTACCAACATCGACGCGCATGAAGCTCCGGGATTAATCTGCGAATAACCAACACAT 641
 DB 576 GTCTCAAGCAACGTTGGAGGATTTTCAAGTGTATGATACATTGAAGAAGAAACTGGTAG 635
 QY 642 ATTTGATCAGAATCGGTTCCATAGAAATCTTTGAGCAACGCGAGACGCTGCTTACGATAT 701
 DB 636 CGATGCTAA-----ACGGAATGAATTTATTAATACAGAGATGCTGCTTACGATAT 689
 QY 702 CATCAAGCGCAAGGCTATATCTCATATGGAATCGCAGCGGGATTAATTCGCATAGTAA 761

PN WO200134809-A2.
 XX 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-US30782.
 XX 09-NOV-1999; 99US-0164258.
 XX (GLAX) GLAXO GROUP LTD.
 XX Kimmerly WJ;
 XX WPI; 2001-316495/33.
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 PS Claim 8; Page 2095-2096; 2188pp; English.
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH5091 to
 CC AAH5098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 3019 BP; 1032 A; 526 C; 381 G; 1080 T; 0 other;
 Query Match 18.9%; Score 183.8; DB 22; Length 3019;
 Best Local Similarity 53.0%; Pred. No. 2.8e-47;
 Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;
 51 AAAAGTTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGCGTATACGTTCTTCT 110
 1792 AAAAGTTGTGTAGTGGAGTGGGTCCGTAGGTTCAAGTTATGCAATTTGCTATGGTGAC 1733
 111 CAGGGCATCGTTTCCGAGATTGTCCTTATCGACGTGAACAAAGACAGAGGGTGA 170
 1732 TCAAGGAATTGCAGATGAATTTGAATTTATGATTTGCAAAAGATAAAGTGAAGCAGA 1673
 171 AAGCATGACCTTAAACACGACGACGACCTTCAATACAAAGGTCTCG-----AGCGGG 221
 1672 CGTTAAGATTAAACCAATGTGACCTTACAGTTCTTCCACAGTACTGTAAAGCTGG 1613
 222 TGATTATCCTGACTCGCGTGGCGGCCCATTTGTTATTTGTCACATGTGGGATTAACCAAAA 281
 1612 AGAATATGAAGATTGTAAGATGACAGATTTAGTTGTTATTACACAGGTGCACCTCAAAA 1553
 282 AAATGGACAAACAGGATGGATCTTGTGCAAAAANTGCCAATTTATGCTGGAAATCAT 341
 1552 ACCGGGTGAAACTCGTTTACAACTTGTGTAAGAAATACTAAATATCAATGAAGATATCGT 1493
 342 CCCCAATGTTGCCAAATATGCTCTCTGTATACCATCTGCTTATTCGCCAGATCTGTGCA 401
 1492 AACTAGTGTATGATAGTGGCTTTGATGGTTTCTTCTTAATGCTGCAACACAGTTGA 1433
 402 TGTTTTGACCTATATAGCTATAAGGGCGTACAGGTTTCCATTAAGCAGAGTATTCGGCTC 461
 1432 TATCTTAACAGTTATGTTAAAGAAGTTACAGGTTTACAGGTTTACAGGTTTACAGGTTT 1373

QY 462 AGGTACAGTCTCGGATCTGCTGTTTAAATACATCTCTCGGAGACACTTCAAGATCTC 521
 DB 1372 TGGTACAGTCTGTTGATAGTGAAGATTTCAGATTTTAAATGAATAAGAAATTAGGTGTTAC 1313
 QY 522 ATCGGACAGCATCGATGCTGTTAATTCGAGAACATGTTGGGTGTCCTGCTCTG 581
 DB 1312 ATCAAGTAGTGTTCAGCTAGCATTTATAGTGAACATGTTGACTCTGAACCTGCACTTTG 1253
 QY 582 GTCTCTTACCAACATCGACGGCATGAAGCTCCGGGATTACTCGGAAAAAGCCAAACCAT 641
 DB 1252 GTCTCAAGCAACAGTTGGAGGTTATTCAGTGTATGATACATTTGAAGAAGAACTGGTAG 1193
 QY 642 ATTTGATCAGATCGTTCCATAGATCTTTCGAGCAACGCGAGCGCTGCTTACCATAT 701
 DB 1192 CGATGCTAA-----AGCAATGAAATTTATATTAACAAGAGATGCTGCTTACCATAT 1139
 QY 702 CATCAAGCGCAAGGCTATATCTATGGAATCGCAGCGGATTACTTCGCATAGTAA 761
 DB 1138 CATTCAGCTAAGGATCTACGTATTATGTTAGTATAGCTCTAGCACTATTACGATTCTAA 1079
 QY 762 GCGGATTTTAGAGGATACAGGATCCACACTTACAGTTTCAA---CGTTGGTGAATTATTT 818
 DB 1078 AGCTTTACTAAATAATGAAATAGTATTTTGACAGTTTCTAGTCAACTTAATGTTCAATA 1019
 QY 819 TGGGTTGACAAATGCTATAAGGCTCCCTACCAACTCAATAAAGTGGGCTCATCA 878
 DB 1018 TGATTTAACGATGTTTATCTTGGCTTACCAACACTTATCAATCAAAATGGTGCAGTTAA 959
 QY 879 AGTGGCTGAACCTTCACTCGATGAGGAAGAAATAGAAATGATGGAAGAAATCAG 931
 DB 958 AATTATGAACACCACTTAATGATAACCACTAGCACTAGCACTAGCACTAGCACTAGCACTAG 906
 RESULT 7
 AAH54429
 ID AAH54429 standard; DNA; 4093 BP.
 XX AC AAH54429;
 XX DT 03-SEP-2001 (first entry)
 XX S. epidermidis genomic polynucleotide sequence SEQ ID NO:3793.
 XX Staphylococcus epidermidis SRI strain; infection; diagnosis;
 XX vaccination; endocarditis; ds.
 XX Staphylococcus epidermidis.
 XX WO200134809-A2.
 XX 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-US30782.
 XX 09-NOV-1999; 99US-0164258.
 XX (GLAX) GLAXO GROUP LTD.
 XX Kimmerly WJ;
 XX WPI; 2001-316495/33.
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 XX Claim 8; Page 1426-1427; 2188pp; English.
 XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors

12 1000 *****CIGARETTES***** 18/07/2001

Query Match 18.9%; Score 183.6; DB 24; Length 1255;
Best Local Similarity 53.2%; Pred. No. 2e-47;
Matches 465; Conservative 0; Mismatches 394; Indels 15;

54 AGTTGTGGTAGTGGAGTGGAGTGGTCTGCGACAGCGTATACGTTGCTTCTCAG 113
 322 AGTAGCACTTATAGGAACGGGTTTCGTTGGGGCAGCTATGCAATTCGCCCTTATGAACCA 381
 114 CGGCATCGTTCCGAGATTGTCCTTATCGAGCTGAACAAAGACAAAGCAGAGGGTGAAG 173
 382 AGGAATAGCAGATGATGATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
 174 CATGACTTAAACCAACGACGACCTTCAATACAAAGTCTCTCTCTCTCTCTCTCTCTCTCT 224
 442 GATGGAATTAATCACGAAAGATTTTCGCGCCGAGCCGATGAATATTTGGTTGGAGA 501
 225 TTATCTGACTGCGCTGGCGGCCATTGTTATGTCACATGTTGGGATTAACCAAAAAA 284
 502 TTATCAAGATTGCAACGCGCGATTTGGTGGTGAATTTGTCAGGGCTTAACCAAAAGCC 561
 285 TGGAACAACAGGATGATCTTCTGCAAAAAATGCCAAATATGCTGGAATCATCCC 344
 562 GGGAGAACAGACTGATCTTGTGACAAATATTAATATCTTCAAAAGTGTGCA 621
 345 CAATGTTGCCAATATGCTCTGATACATCTGCTTATGTCACGAATCTCTGTCGATG 404
 622 TTCTGTGATGAATCCGGATTTGATGGGTTTTCTTGTGCAACGACCAAGTGGATAT 681
 405 TTTCACCTATATTAGCTATAGGCGTCAAGGTTTCCACTAAGCAGATTTATCGGCTCAGG 464
 682 TTAAACGTATGCTACTTTGGAATTTAGCGGTTTACCGAAAGAGCGGGTATTCGGCTCAGG 741
 465 TACAGTTCTGATGACTGCTCTTTTAAATACATCTCGGAGACACTTCAAGATCTCATC 524
 742 AACGATCTTGATACAGCAAGATTCGCTTCTGCTAAGTGAATATTTCAAGTGGCTC 801
 525 GGACAGCATGATCGCTGTGTAATGAGAACATGTTGATGATGATGATGATGATGATGATGAT 584
 802 GACCAATGTATCATGCTATATTTATGCGAGCATGGGGATACAGAGCTGCTGTTGGAG 861
 585 TCTTACCAACATCACGCGCATGAGCTCCGGATTTACTGCGMAAAGCCCAACCATATT 644
 862 CCATGCGGAATGGAAGCATTCAGTTGAGCAATATTTGATGCA---AACGATACTA 918
 645 TGATCAGATGCGTTCCATAGAATCTTTTGAGCAACGCGAGACGCTCTTACGATATCAT 704
 919 TAGAAAAGAGATTAGACAAATATCTTTGTTAATGTTGCTGATGCGGCATATCAATCAT 978
 705 CAACGCAAGGCTATCTTATATGAAATCGAGCGGATTTACTTTCGATAGTAAGG 764
 979 TGAAAAAAGGGGCAACGATTTACGGCATTTGCAATGGGATTTAGTCCGATCATCTCGTC 1038
 765 GATTTTAGAGGATACAGGATCCACATTTACAGTTTCAAC---CGTTGCTGATTTTGG 821
 1039 TATTTTGCACATGAAATGCGCATCTTAAACGTTTCTGCTCATTTGGACGCCAATATGG 1098
 822 GGTGAAACAATTTGCTATAGCGTCCCTTACCAAACTCAATAAAGTGGGGCTCATCAAGT 881
 1099 CGAACGAAATGTTTATATGCGGTGCTGCGCATTTCAACCGAAACGCTATTCGTGAAT 1158
 882 GGCTGAACCTTCACTCGATGAGAGGAATAAGAA 915
 1159 GATGGAATTGACGCTAAATGAACAGAACACAA 1192

RESULT 9

AA13275/c

ID AA13275 standard; DNA; 13154 BP.

XX

AC

XX

XX

DT

XX

DE

XX

KW

vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.

WO9850555-A2.

12-NOV-1998.

04-MAY-1998; 98WO-US08985.

14-NOV-1997; 97US-0066009.

06-MAY-1997; 97US-0044031.

16-MAY-1997; 97US-0046655.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;

WPI; 1999-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection.

Claim 1; Page 1444-1450; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX1319 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection.

Sequence 13154 BP; 4253 A; 2268 C; 2870 G; 3762 T; 1 other;

Query Match 17.8%; Score 173; DB 20; Length 13154;

Best Local Similarity 51.7%; Pred. No. 1.6e-43;

Matches 473; Conservative 0; Mismatches 430; Indels 12; Gaps 3;

QY 51 AAAAGTTGTGTAGTGGAGTGGAAAGTGTGGGTCTGCCACAGCGTATACGTTGCTTCT 110

DB 6674 AAAAGTAAATTTAGTGGGACGGTCCGTAGTGTCTAGCTATGCTTTGCTTAGTAAC 6615

QY 111 CAGCGCATCGTTTCCGAGATTGCTCTTATCGACGTGAACAAAGACAGAGGGTGA 170

DB 6614 TCAGAAATATGCTCAAGAAAGTTGGGATTTATGATATTAATGTACCAAAAACCTGAAGAGA 6555

QY 171 AAGCATGCTAAACACGACGACAC-----CTTCAATACAAAGTCTCGACGGGTGA 224

DB 6554 CGGTTGGACTTATCTCAGCATTTAGCTTTCTCTCTTAAATAATCTATGCTGTAC 6495

QY 225 TTATCTGACTGCGCTGGCGGCCCATTTGTTTGTACATGTGGGATTAACCAAAAAA 284

DB 6494 TTATGACGATTGCGATGATGACACTTAGTTGTCTTAAACAGTGGTGGCGCTCAAAACC 6435

QY 285 TGGACAAAACAGGATGCTTCTGCAAAAAAATGCAACATTATGCTGGAATCATCCC 344

DB 6434 AGCGAAACTCGTTTAGACTTAGTTTATATAAAATTTGAAATTAATAAGAAATCGTTAC 6375

QY 345 CAATGTTGCCAATATGCTCCTGATACCATCTCTGCTTTATGCGCAATCTCTGCTGATGT 404

DB 6374 ACAAATGTTGATCTGGTTTCAACGGTATCTTTTAGTTGCGCAACCCAGTTGATAT 6315

QY 405 TTTGACCTATATTAGCTATAAGCGCTCAGGGTTTCCACTAAGCAGAGTTATCGGCTCAGG 464

Enterococcus faecalis; contig; detection; Enterococcal infection;

Db 6314 TTTCAGCTTATTCACCTTGGAAATCTCTGGCTTCCGAAAGAACGAGTAATCGGTTCCAGG 6255
 Qy 465 TACAGTTCTGATCTCTCGTTTAAATACATCTCGAGAGCACCTTCAAGATCTCATC 524
 Db 6254 AACTTCACTAGATCTCTCGTTTCCGTCAGCAATTCGCCAATAGTTCAGCTTGATGC 6195
 Qy 525 GGACAGCATCGATCGCTGTGTAAATTTGGAGAACATGTGTATTCGGGTGTGCTGTCTGGTC 584
 Db 6194 ACGAATGTCCATCGCTACATCTTAGGGAACACGGAGATACAGAAATCCAGTTTGGTC 6135
 Qy 585 TCATTACCAATCGACGGCATAGCTCCGGATTAATCGGAAATTAATCGGAAAGCCAAACCATATT 644
 Db 6134 ACATGCCAATGTCTCGCTTACAAAT---TTACGAATGGGTGAAAAAATAATCTGACGT 6078
 Qy 645 TGATCAGAATGCGTTCCATAGATCTTTTGAGCAAAACGCGAGACGCTCTTACGATATCAT 704
 Db 6077 CGATGAAGAAGCAATGTTTATTTATCTTCAAGTACGCGACGCTCTTACAAATCAT 6018
 Qy 705 CAAGCGCAAAAGGCTATCTTATATGGAATCGCAGCGGGATTAATTCGCATAGTAAAGGC 764
 Db 6017 CGAGAAAAAGGAGCTACTTCTATGGAATCGCGTTTGCATAGCGGTATCACTAAAGC 5958
 Qy 765 GATTTTAGAGATACAGATCCACACTTACAGTTTC---AACCGTTGGTGAATTTTGG 821
 Db 5957 TATCCTAAACGATGAAACCTCTGTGTTACCAATATCTGTTTATTAGAGGTGAATATGG 5898
 Qy 822 GGTGAAACAATTTGCTATAGCGCTCTTACCAACTCAATCAAAAGTGGGCTCATCAAGT 881
 Db 5897 TCMAAGCATATTTATATCTCGTGCACCGCATCATCAACCGCAAGGATTAACCAAGT 5838
 Qy 882 GGCTGAATTTCACTCGATGAGAAGAAATAGAAATTCATGGAATAATCAGTATGATCAGAT 941
 Db 5837 CATTTGAATTTCCATTAACAGATCTGCAACGAATAATGAGACCTCTCTCTGTCATT 5778
 Qy 942 CAATCAGTATGGA 956
 Db 5777 AAAAGAAGTTATTGA 5763

RESULT 10

AAV74735

ID AAV74735 standard; DNA; 3264 BP.

XX AC

AAV74735;

16-MAR-1999 (first entry)

Staphylococcus aureus contig SEQ ID #424.

Computer readable medium; vaccine; S.aureus infection; immunodetection;
 cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 skin infection; surgical wound infection; scalded skin syndrome;
 toxic shock syndrome; ds.

Staphylococcus aureus.

Key Location/Qualifiers

misc_feature 1441..1500

/*tag= a

/note= "these bases represent a line of missing text in
 the sequence listing in the specification. They
 are included to maintain the nucleotide numbering
 given in the specification for this DNA sequence"

misc_feature 3241..3264

/*tag= b

/note= "these bases represent a line of missing text in
 the sequence listing in the specification. They
 are included to maintain the nucleotide numbering
 given in the specification for this DNA sequence"

EP786519-A2.

XX

PD 30-JUL-1997.

XX 07-JAN-1997; 97BP-0100117.

XX 05-JAN-1996; 96US-0009861.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;

PI Rosen CA;

XX WPI; 1997-374922/35.

XX Polynucleotide(s) and proteins derived from Staphylococcus aureus

PT stored on computer readable medium and used in the production of

PT anti-S.aureus vaccines

XX Claim 1; Page 1324-1325; 3271pp; English.

XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 of the invention. The DNA sequences are recorded on a computer readable
 medium, preferably selected from a floppy or hard disk, random access
 memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 the S.aureus DNA sequences allows putative functions to be assigned so
 that protein-encoding or regulatory regions of commercial, therapeutic or
 industrial importance can be obtained. Specifically, sequences which are
 likely to encode antigens have been identified and these polypeptides can
 be used in a vaccine composition against S.aureus infection. The
 polypeptides can also be used in a kit for the immunodetection of
 S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 skin and surgical wound infections, scalded skin syndrome, toxic shock
 syndrome, etc. Organisms transformed with the DNA sequences can be used
 for recombinant production of the polypeptides. The new DNA sequences
 (and their fragments) are useful as primers or probes for isolating
 homologues of any of the S.aureus DNA sequences contained on the
 computer readable medium.

XX Sequence 3264 BP; 1063 A; 462 C; 656 G; 996 T; 87 other;
 Query Match 17.8%; Score 172.6; DB 18; Length 3264;
 Best Local Similarity 52.2%; Pred. No. 1e-43;
 Matches 469; Conservative 0; Mismatches 409; Indels 21; Gaps 3;

SQ

Qy 51 AAAAGTTGTGTAGTGGAGTGGAGTGTGGTCTGCCACAGCGTATACGTTGCTTCT 110
 Db 412 AAAGTTGTATTAATCGGATGGATCTGTAGATCAAGTATGCTTCCATATGGTTAC 471

Qy 111 CAGCGCATCGTTTCCGAGATTCCTTATTCGACGTGAACAAAGACAGAGGGTGA 170
 Db 472 GCAAGGTGTGCTGATGAATTTCTTAATTTAGACATTCGAAAGACAAAGTAAAGCAGA 531

Qy 171 AAGCATGAGCTTAAACACGACGACCA-----CCTTCAATATCAAGGTCTCGAGCGG 221
 Db 532 TGTTCAAGATTTAAACCATGGTACAGTCCACAGTCTCTCACCAGTTGATGGAAGCAGG 591

Qy 222 TGATTATCTCTGCTGCTGGCGGCCATTGTTATTGTCACATGTGGGATTAACCAAAA 281
 Db 592 TGAATACGAAGACTGTAAGATGCAGATTTAGTTGTTATTACAGCTGGTGACCTCAAAA 651

Qy 282 AATGACAAAACAAAGGATGGATCTTCTGCAAAAAATGCCAAATATATGCTGGAATCAT 341
 Db 652 GCCAGGTGAACACAGTTTACAAATAGTTGAAAAAATACTAAGATATGAAGAGCATCGT 711

Qy 342 CCCCAATGTGGCAAAATATGCTCTGATACCATTCCTGCTTATTGCGACGAATCTGTGCA 401
 Db 712 TAAGAGTGTATGGATAGTGGCTTTGATGGATATTTCTTAATCGCGCAAAACCTGTAGA 771

Qy 402 TGTTTTGACCTATATTAGCTATTAAGCGGTTCAGGGTTTCCACTAAGCAGAGTATCGGCTC 461
 Db 772 CATTTTAAACAAGATTTGTAAGAAATATATCTGGATTACCAGAGAGCGGTGTATCGGTT 831

Qy 462 AGGTACAGTTCTGGATACTGCTCGTTTAAATACATCCTCGGAGAGCACTTCAAGATCTC 521

Db 741 TATCTTTGATGATGAAATCTGTCTCTCGCTCTCTGTTTCCAGAGGCCAATACGA 800
 Qy 819 TGGGTTTGAACAAATTCCTATAAGCGTCCCTACCAAACTCAATAAAGTGGGCTCATCA 878
 Db 801 AGGTGTTGAAGATGCTATATTTGTTCAACAGCTATCGTTGGAGCGTATGGAATTTGTCG 860
 Qy 879 AGTGGCTGAATCTTCACTCGATGAGAGGAAATAGAAATTCATGGAATAATCAGCTAGTCA 938
 Db 861 TCCAGTAAACATTTCCACTTAACGATGCTGAATTACAAAATGCAAGCCTCTGCAATCA 920
 Qy 939 GATCAAAATCAGTATTCA 956
 Db 921 ATTGAAGCTATCATTTGA 938

RESULT 12

AAZ09139

ID AAZ09139 standard; DNA; 945 BP.

XX AC

AAZ09139;

XX XX

18-OCT-1999 (first entry)

XX XX

DE B. flavum lactate dehydrogenase DNA.

XX XX

Lactate dehydrogenase; destruction; lactic acid; ss.

XX XX

OS Brevibacterium flavum.

XX XX

FH Key Location/Qualifiers

FT CDS 1..945

FT FT /*tag= a

FT FT /product= "lactate dehydrogenase"

XX XX

PN JP11206385-A.

XX XX

PD 03-AUG-1999.

XX XX

PF P-PSDB; AAY25997.

XX XX

PR 28-JAN-1998; 98JP-0030594.

XX XX

PA (MITU) MITSUBISHI CHEM CORP.

XX XX

DR WPI; 1999-486360/41.

XX XX

DR P-PSDB; AAY25997.

XX XX

PT New lactate dehydrogenase gene and strain destroying gene - useful

XX XX

PT for formation of lactic acid

XX XX

PS Claim 2; Page 10-11; 13pp; Japanese.

XX XX

CC This invention describes the isolation of a novel lactate dehydrogenase protein from Brevibacterium flavum strain MJ-233. The invention also describes a microbial strain destroying the lactate dehydrogenase gene of a microbe in which the lactate dehydrogenase gene is destroyed by a homologous recombination of the above DNA or the above recombinant vector DNA with the lactate dehydrogenase gene on the chromosome DNA of the microbe cell and a method for the preparation of an amino acid or an organic acid in which the above strain destroying the lactate dehydrogenase gene is cultured in a medium and the amino acid or the organic acid (except lactic acid) is collected from the culture.

CC Formation of lactic acid in the preparation of an amino acid and an organic acid can be decreased with no control of oxygen concentration during culture. This sequence encodes the lactate dehydrogenase protein described in the specification.

XX XX

SQ Sequence 945 BP; 238 A; 285 C; 237 G; 185 T; 0 other;

Query Match

Best Local Similarity 16.0%; Score 155.8; DB 20; Length 945;

Matches 457; Conservative 0; Mismatches 422; Indels 18; Gaps 3;

DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.
 XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW

RESULT 13

AA71424

ID AA71424 standard; DNA; 1065 BP.

XX AC

AA71424;

XX XX

DT 30-APR-2001 (first entry)

XX XX

DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.
 XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW

Qy 52 AAAGTTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGCGTATACGTTGCTTCTC 111
 Db 22 AAGATTGTCTTATTTGCGCGCAGGAGATGTTGGATTGTCATACGCATACGCCTGATCAAC 81
 Qy 112 AGCGGATCGTTTCCAGATTTGCTTATTCGACGTGAACAAAGACAAAGCAGAGGGTGAA 171
 Db 82 CAGGGATCGCAGATCACCTTGGATCATCGACATCGATGAAAGAACTCGAAGGCAAC 141
 Qy 172 AGCATGGACTTAAACACGCA-----GCACCTTCAATACAAAGGTTCTCGAGCGGT 222
 Db 142 GTCATGGACTTAAACCATGTTGTTGGGCGCATTCGCGCACCCCGCTGCACAAAGGC 201
 Qy 223 GATTATCTCACTGCGCTGCGCGGCATTGTTATTGTACATGTGGGATTAAACCAAAAA 282
 Db 202 ACCTACGCTGACTGCGAGGACGAGCCATGTTGTCATTTGTGCCGCGCAGCCAAAG 261
 Qy 283 AATGGACAAACAGGATGATCTTGTGCAAAAAATGCAAAATTTATGCTGGAATCATC 342
 Db 262 CCAGGCGAAATCGCCTCCAGCTGCTGGAGCAAAAAAGTCAAGATTATGAAGTCCATCGTT 321
 Qy 343 CCCAATGTTGCCAAATATGCTCTGATACCATCTCTGTTATTGCGCACGATCCCTGCGAT 402
 Db 322 GCGGATGTCATGGCCAGCGGATTTCGACGGGATCTTCTCGTAGCCTCCAACCCAGTGAT 381
 Qy 403 GTTTTGACCTATATTAGCTATAAGGCGTCAGGGTTTCCACTAAGCAGAGTTATCGGCTCA 462
 Db 382 ATCTCTACCTACGAGTGTGGAATTTCTCGCGCTGGAATGGNACCGCGTATCGGCTCC 441
 Qy 463 GGTACAGTTCTGGATACTCTCGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCA 522
 Db 442 GGAATCTCTGGACTCCGCTAGATTCCGCTACATGCTCGGCGAACTCTATGAAGTGGA 501
 Qy 523 TCGGACAGCATCGATGCTGTTGTAATTGAGACATGTTGCGGGTGTGCTGCTGCTGG 582
 Db 502 CCAAGCTCCGTCACGCTTACATCATCGGCGAACACGCGGACACTGAACCTTCCAGTCTG 561
 Qy 583 TCTCTTACCAACATCGACGCGCATGAAGCTCCCGGATTACTGCGAAAAAGCCACACATA 642
 Db 562 TCCTCGCGACCATCGCAGCGGTATCGCTTAG-----CGCATGTAGACAAAGACCCA 615
 Qy 643 TTTGATCAGATGCGTTCCATAGATCTTTGAGCAAAACGCGAGACGCTGCTTACGATATC 702
 Db 616 GAGCTTGGGGCGCTCTAGAGAAAAATTTTCGAAGACACCGCGACGCGCTATCATATC 675
 Qy 703 ATCAAGCGCAAGGCTATATCTTATGAAATCGACGCGGATTAATTCGCATAGTAAAG 762
 Db 676 ATCGACGCAAGGCTCCACTTCTACGGCATCGGATGGGTCTTGTCTGCGCATCACCCGC 735
 Qy 763 GCGATTTTAGAGGATACAGGATCCACACTTACAGT---TTCACCCGTTGGTGATTATTTT 819
 Db 736 GCAATCTTACAAAACCAAGACGTTGCGTCCAGTCTCTGCACTGCTCCACGGTGAATAC 795
 Qy 820 GGGTTTGAACAAATGCTATAAGCGTCCCTACAAACTCAATAAAGTGGGGTCTATCAA 879
 Db 796 GGTGAGGAGACATCTACATCGCACCCCGCAGAGTAGTAAACCGCGAGGCGATCCGCGC 855
 Qy 880 GTGGCTGAACTTCTACTCCATGAGAGGAAATAGATTGATGAAAAAATCAGCTAGT 936
 Db 856 GTTGTGCAACTAGAAATCACGGACCATGAGATGGAACGCTTCAAGCATTCCTCCGCAAT 912

[illegible]

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 XX
 XX Disclosure; SEQ ID NO: 7069; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 other;
 Query Match 15.9%; Score 154.2; DB 22; Length 309400;
 Best Local Similarity 50.8%; Pred. No. 8.1e-37; Indels 18; Gaps 3;
 Matches 456; Conservative 0; Mismatches 423;
 Qy 52 AAGTGTGGTGTGGAGTGGGAGTGTGGGCTGCCAGCGTATACGTTGCTTCTC 111
 Db 113369 AAGATTGTCTCTATTGGCGGAGGAGATGTTGGAGTTCATACGCTACGCACTGATCAAC 113310
 Qy 112 AGCGGCTGTTTCGGAGATGTCCTTATGACGTGACAAAGCAAGAGAGAGGGTGAA 171
 Db 113309 CAGGGCAGTGGCAGATCACTTGGCATCATGACATGATGAAAGAAACTCGAAGGCAAC 113250
 Qy 172 AGCATGGAATTAACACGCA-----GCACCTTCAATACAAAGTCTCGAGCGGGT 222
 Db 113249 GTCATGGAATTAACACGCTGTTGTGGGCCGATTCGCCACCCGGTCCACCAAGGC 113190
 Qy 223 GATTATCTGCTGCTGGCGGCCGCTATTTATGTCACATGTGGGATTAACCAAAAA 282
 Db 113189 ACCTAGCGTACTGGAAGACGCGCATGTTGTCATTTGTGCGCGCGCAGCCCAAAAG 113130
 Qy 283 AATGACAAACAGATGGATCTTGTGTCAAAAAATGCCACATATGCTGGAATCATC 342
 Db 113129 CCAGCGGAGACCCGCTCCAGCTGGTGACAAAAACGTCAAGATTATGAAATCCATCGTC 113070
 Qy 343 CCCAATGTGCAAAATATGCTCTGATACCATCTGCTTATTGTCACGAATCTCTGTCGAT 402
 Db 113069 GCGGATGTCTGACAGCGGATTCGACGGCATCTCTCTGCGGCTCCACCCAGTGGAT 113010
 Qy 403 GTTTTGACCTATATAGCTATAGCGGCTCAGGGTTTCCACTAACAGAGTATCGGCTCA 462
 Db 113009 ATCTGACCTACGCGATGTGGAATTTCTCGGCTTGAATGGAACCGCGTATCGGCTCC 112950
 Qy 463 GTTACAGTCTGGATCTGCTCGTTTAAATACATCTCGGAGAGACTTCAAGATCTCA 522
 Db 112949 GGAATGTCCTGGAATCTCGCTCGATTCGCTACATGCTGGCGAACTCTACGAAGTGGCA 112890
 Qy 523 TCGGACAGCATCGATCTGTAATTGGAGAACATGCTGATTCGGGTGTCCTGTCTGG 582
 Db 112889 CCAAGCTCCGTCACGCTTACATCATCGGCGAACACGCGGACACTGAACTTCCAGTCTG 112830
 Qy 583 TCTCTTACCAATGACGCGCATGAAGCTCCGGGATTAATGCGAAAAAGCCACATA 642
 Db 112829 TCCTCCGCGACCATCGAGGGGTATCGCTTAGCCGAATGCTGGACAAAGACCCAGAGCT- 112771

Qy 643 TTTGATCAGATCGGTTCCATAGATCTTTGAGCAAAACGGAGACGCTGCTTACGATATC 702
 Db 112770 -----TGAGGGCGGCTCTAGAGAAAATTTTCGAAGACACCCGCGACGCTGCTATCACATT 112716
 Qy 703 ATCAAGCGCAAGGCTATCTTCATATGGAATCGCAGCGGGATTACTTTCGATAGTAAAG 762
 Db 112715 ATCGAGCGCAAGGCTTCCTTCTACGGCATCGGATGGGTCTTCTGCTGCAATCACCAGC 112656
 Qy 763 GCGATTTTAGAGGATACAGGATCCACACTTACAGT---TTCACCGGTTGGTGAATTTT 819
 Db 112655 GCAATCTCTGAGAACCAAGAGGTTGCAGTCCAGTCTCTGCACTGCTCCACGGTGAATAC 112596
 Qy 820 GGGGTTGAACAATTCCTATTAAGCGTCCCTACCAAACTCAATAAAAGTGGGCTCATCAA 879
 Db 112595 GGTGAGGAAGACATCTACATCGCACCCCGAGCTGTGGTGAACCGCGAGGCAATCCCGCGC 112536
 Qy 880 GTGGCTGAACCTTTCACCTCGATGAGAAGAAATAGAAATGATGAAAAATCAGCTAGT 936
 Db 112535 GTTGTGAACTAGAAATCACCCAGCAGAGATGGAAGCTTCAAGCATTCGCGCAAT 112479

Search completed: July 31, 2003, 09:47:36
 Job time : 286 secs

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 08:56:31 ; Search time 62 Seconds
(without alignments)
4807.900 Million cell updates/sec

Title: US-09-992-430B-21

Perfect score: 972

Sequence: 1 atgttcaagatacaagtc.....ttgagcatctggagatcaat 972

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCITUS COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183.8	18.9	993	4	US-09-134-001C-1491
2	153.6	15.8	5278	4	US-08-961-527-227
3	147.2	15.1	5449	4	US-09-546-990-1
4	125	12.9	1661	4	US-09-166-350-31
5	109.8	11.3	1260	4	US-09-166-350-22
6	101.2	10.4	1240	1	US-08-869-506-1
7	101.2	10.4	1240	3	US-09-128-967-1
8	93.8	9.7	1116	4	US-09-535-381-1
9	93.8	9.7	6072	4	US-09-535-381-3
10	89.2	9.2	1912	1	US-08-270-013B-1
11	89.2	9.2	1912	1	US-08-838-418-1
12	81	8.3	978	4	US-09-134-001C-2696
13	79.8	8.2	566	4	US-09-328-111-455
14	74.2	7.6	5024	1	US-08-920-812-7
15	74.2	7.6	5024	1	US-08-920-827-7
16	74.2	7.6	5024	1	US-08-921-177-7
17	74.2	7.6	5024	1	US-08-362-577-7
18	74.2	7.6	5024	2	US-08-920-828-7
19	62.2	6.4	519	4	US-09-222-575-160
20	59	6.1	1679	3	US-08-676-882-1
21	58.4	6.0	951	5	PCT-US94-03796-1
22	52.4	5.4	497	4	US-09-370-838-129
23	51.4	5.3	493	4	US-09-370-838-181
24	36.2	3.7	429	4	US-09-071-035-89
25	36	3.7	87350	3	US-08-781-891-79
26	36	3.7	87543	4	US-09-791-211-3
27	35.4	3.6	259	4	US-09-071-035-91

ALIGNMENTS

RESULT 1

US-09-134-001C-1491
; Sequence 1491, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1491
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1491

Query Match 18.9%; Score 183.8; DB 4; Length 993;
Best Local Similarity 53.0%; Pred. No. 2.2e-49;
Matches 473; Conservative 0; Mismatches 402; Indels 18; Gaps 3;

28	34.4	3.5	471	4	US-09-134-001C-1397	Sequence 1397, Ap
C 29	34	3.5	7218	1	US-08-232-463-14	Sequence 14, Appl
30	33.8	3.5	608	4	US-09-328-111-532	Sequence 532, App
31	33.8	3.5	619	4	US-09-328-111-400	Sequence 400, App
C 32	33.8	3.5	2912	4	US-09-307-143-3	Sequence 3, Appl1
33	33.4	3.4	477	1	US-08-403-866-13	Sequence 13, Appl1
34	33.4	3.4	2231	1	US-08-403-866-14	Sequence 14, Appl1
35	33.4	3.4	12720	1	US-08-403-866-11	Sequence 11, Appl1
36	32.8	3.4	3292	4	US-09-336-447A-14	Sequence 14, Appl1
37	32.8	3.4	19227	3	US-09-090-793-13	Sequence 13, Appl1
38	32.8	3.4	40138	3	US-09-090-793-12	Sequence 12, Appl1
39	32.2	3.3	1203	1	US-08-602-010A-7	Sequence 7, Appl1
40	32.2	3.3	1203	3	US-08-680-726A-7	Sequence 7, Appl1
41	32.2	3.3	1203	3	US-09-092-409-7	Sequence 7, Appl1
42	32.2	3.3	5495	1	US-08-602-010A-1	Sequence 1, Appl1
C 43	32.2	3.3	5495	1	US-08-602-010A-2	Sequence 2, Appl1
44	32.2	3.3	5495	1	US-08-680-726A-1	Sequence 1, Appl1
C 45	32.2	3.3	5495	1	US-08-680-726A-2	Sequence 2, Appl1

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Qy 402 TGTTTTCACCTATATTAGCTATATAAGCGCTCAGGGTTTCCCTAAGACAGAGTTATCGGCTC 461
Db 420 TATCTTAACAGCTTATGTTAAAGAGTTACAGGTTTACAGCTGAACGTGTTATGTTGTTTC 479
Qy 462 AGGTACAGTGTCTGATACCTGCTGTTTAAATACATCCTCGGAGAGCACTTCAAGATCTC 521
Db 480 TGGTACAGTGTCTGATAGTGAAGATTGAGATTTAATAAGTAAAGAAATTAGGTGTAC 539
Qy 522 ATCGGACAGCATCGATCGCTGTGTAATTTGGAGACATGGTGATTCGGGTGCTGCTGTCG 581
Db 540 ATCAAGTAGTGTTCACGCTAGCATTTATAGGTGAACATGGTGACTCTGAACCTTCAGTTG 599
Qy 582 GTCTCTTACCAACATCGACGCGCATGAAGCTCGGGATTACTGCGAAAAGCCACACAT 641
Db 600 GTCTCAAGCAACGTTGGAGGTATTTGAGTGATGATACATTTGAAAGAAAGAACTGGTAG 659
Qy 642 ATTTGATCAGAAATCGTTTCCATAGAAATCTTTTGAACAAACGCGAGACGCTGCTTACGATAT 701
Db 660 CGATGCTAA-----AGCGAATGAAATTTATATTAATACAAAGAGATGCTGCTTACGATAT 713
Qy 702 CATCAAGCGCAAGGCTATCTTATATGAAATCGGAGCGGGATTACTTCGCATAGTAA 761
Db 714 CATCAAGCTAAAGGATCTACGTATTTATGTTATGTTATGCTTACGACTATTTACGTATTTCTAA 773
Qy 762 GCGGATTTTACAGGATACAGGATCCACACTTTACAGTTTCAA---CCGTTGGTGATTTATTT 818
Db 774 AGCTTTACTAAATGAAATAGATATTTTGACAGTTTCTAGTCAACTTAATGTCATA 833
Qy 819 TGGGTTTGAACAAATGCTATAGCGTCCCTTACCAAACTCAATAAAGTGGGGCTCATCA 878
Db 834 TGGATTTAAACGATGTTATCTTGGCTTACCACACTTATCAATCAAAATGTCAGTTAA 893
Qy 879 AGTGGCTGAATTTCACTCGATGAGAGGAATAGAAATGATGCAAAATCAG 931
Db 894 AATTTATGAACACCATTAATATGATAAGAACTACAATTTACTAGAAAAATCAG 946

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RESULT 2

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US-08-961-527-227/c
; Sequence 227, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:

```

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; LENGTH: 5278 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-227
Query Match 15.8%; Score 153.6; DB 4; Length 5278;
Best Local Similarity 50.6%; Pred. No. 3e-39;
Matches 484; Conservative 0; Mismatches 454; Indels 18; Gaps 4;
Qy 16 AGTCTCAAGCAGTAAGAACTGATGCCAAAACAGTAAAGTTGTGTAGTGGAGTGGGA 75
Db 5236 ATGTTTAAACAATGATCTTCACTAAACAACAACAAAAAGTTATCTCTGTGCGTGTGGT 5177
Qy 76 AGTGTGGGTCTGCCACAGGTATAGTTGCTTCTCAGCGGCATCGTTTCCGAGATTGTC 135
Db 5176 GCTGTAGGTTCACTTTACGCTTTTGACCTTTTAAACCAAGGAATGCAACAAGAGCTTGA 5117
Qy 136 CTTATCGAGCTGAACAAA-----GACAAAGCAGAGGGTGAAGCATGGAATTTAAACCCAC 189
Db 5116 ATTATCGAAATTCACAAATTCGATGAAGAAAGCTGTTGGTGATCGGCTTGACCTTAGTCAC 5057
Qy 190 -----GCACACCTTTCAAAATCAAGGCTCTCGAGCGGGTGAATTTCTGATCGGCTGGC 243
Db 5056 GCGCTTGCCTTCACTTCACTAAAAAAATCTATGACAGCTCAATCTCTGACTGTGCAGAC 4997
Qy 244 GCGGCCATTTGTTATGTCATGTCAGATTAACCAAAAAAATGGAACAACAAGATGGAT 303
Db 4996 GCTGACCTTGTGTGATCACTGCGAGTGCACTTCAAAAAACGAGTGAAACTCGCTTTGAC 4937
Qy 304 CTTGCTGCAAAAAAATGCCAACATTTATGCTGGAATCATCCCCAATGTTGCAAAATATGCT 363
Db 4936 CTTGTAGGTAAACACCTTGTCTATCAACAATCAATGTAATCAAGTTGTTGAATCTGGT 4877
Qy 364 CTGTATACCATCTCTGCTTATGTCACGAATCTGTGTCGATGTTTGTGACCTATATAGCTAT 423
Db 4876 TTCAAGAGTATCTTCTCTGTTGCTGTAACCCAGTTGACGTTTTGACTTACTCAACTGG 4817
Qy 424 AAGGCGTCAGGTTTCCACTAAGCAGATTTATCGGCTCAGGTACAGTTCTTGGATCTGCT 483
Db 4816 AAATCTCTGTTTCCCTTAAAGAACGCTTATCGGTTCAAGTACTTCACTTGTACTGACT 4757
Qy 484 CGTTTTAAATATACATCTCGGAGAGCACTTCAAGATCTCATCGGACAGCATTCGATGCTGT 543
Db 4756 CGTTTCCGTCAGCACTTCTGCTGAAAAATTTGGATGTGATGCTGTTCAAGTGCAAGCTAC 4697
Qy 544 GTAATTTGGAGAACATGCTGATTCGGGTGTCGCTGCTGCTCTTACCAACATCGACGGC 603
Db 4696 ATCATGGGTGAACACAGGTGACTCTGAGTTGCTGTTTGGTCAACGCTAACATCGCTGGT 4637
Qy 604 ATGAAGCTCGGGATTACTCGGAAAAGCAACACATATTTGATCAGATGCTTCCAT 663
Db 4636 GTAAA---CCTTGAAGAAATTCCTTAAAGACACTCAAAATGTTCAAGAGCTGAATGATT 4580
Qy 664 AGAATCTTTGAGCAAAACGCGAGACGCTGCTTACGATATCATCAAGCGCAAGAGCTACT 723
Db 4579 GAATTTGTCGAAGGTGTTCTGTGATGAGCTTACATCATCAACAAAAAGGTGCAACA 4520
Qy 724 TCATATGGAATCGCAGCGGATTTACTTTCGATAGTAAAGCGGATTTTAGAGGTACAGGA 783
Db 4519 TACTAGCGTATCGCAGTAGCCCTTGTGCTGATCACTAAAGCAATCTCTGACGATGAAC 4460
Qy 784 TCCACACTTTACAGTTTC---AACCGTTGGTATTATTTGGGGTGAACAAAATTTGCTATA 840
Db 4459 GCAGTACTTCCACTTTTCAAGTAATTTCCAAAGAGGTCAATACGAGAGTTGAGAAATGCTTATC 4400
Qy 841 AGCGTCCCTTACCAAACTCAATAAAAGTGGGGCTCATCAAGTGGCTGAACTTTTCACTCGAT 900
Db 4399 GGTCAACACAGCTGTTGTGTTGGTGCACATGTTATCGTTTCGTCAGTAAATATATCCCAATCAAC 4340
Qy 901 GAGAAGGAATAGAAATTTGATGGAATAATTCAGTATGATGATCAATCAATCAGTATTGA 956
Db 4339 GACGCGAGAACTCAAAAAATGCAAGCATCTGCTTAAAGAAATTTACAAAGCTATCATTTGA 4284

```

RESULT 3

US-09-546-990-1/c
; Sequence 1, Application US/09546990
; Patent No. 6346397
; GENERAL INFORMATION:
; APPLICANT: Wilding, Edwina Imogen
; APPLICANT: Gwynn, Michael T.
; APPLICANT: Vasey, Sandra Y.
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: gyzA
; FILE REFERENCE: GM10138
; CURRENT APPLICATION NUMBER: US/09/546,990
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/128,991
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5449
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(5449)
; OTHER INFORMATION: n = A,T,C or G
US-09-546-990-1

Query Match 15.1%; Score 147.2; DB 4; Length 5449;
Best Local Similarity 50.7%; Pred. No. 3.6e-37;
Matches 485; Conservative 2; Mismatches 450; Indels 19; Gaps 5;

QY 16 AAGTCTCAAGCAGTAAGAACTGATGCCAAACAGTAAAGTGTGGTAGTGGGAGTGGGA 75
DB ATGKTTAAACATGACTYRACCTAAACACACAAACAAAGTTATCTTGTGGTGTGGT 2240

QY 76 AGTGTGGGTCTGCCAGCGTATACGTCTTCTCAGCGGCATCGTTTCCGAGATTGTC 135
DB GCTGTAGTTCATCTTACGCTTTTGCACTGTTTAAACCAAGAAATGCAACAGACTTGA 2180

QY 136 CTATCGACGTGACAAA-----GACAAAGAGAGGTGAAAGCATGGAATTAACACCAC 189
DB ATTATCGAAATTCACAAATTCGATGAAAAGCTGTTGGTATGCGCTTGACCTTAGTCAC 2120

QY 190 -----GCAGCAGCTTCAAAATACAAAGTCTCGAGCGGTGATTATCTGACTCGGTGGC 243
DB GCCCTTGCTTCACTTCACTTAAACAAATCTATGAGCTCAATCTCTGACTGTGCAGAC 2060

QY 244 GCGGCCATTGTTATTTGTCATGTGGGATTAACCAAAAAATGGAACAAACAGGATGGAT 303
DB GCTGACCTTGTGTATCACTGCGAGGTGCACCTCAAAAAACAGGTGAACCTGCTTGAC 2000

QY 304 CTTCCTCAAAAAATGCCAATATGCTGGAATCATCCCAATCATCCCAATGTGCAAAATATGCT 363
DB CTTCGTAGGTAAACCTTGTCTATCAACAAATCAATCGTAACTCAAGTTGTGAATCTGGT 1940

QY 364 CTTGATACCACTCTGCTTATTGCCAGCAATCTCTGTCATGTTTGGACCTATATTAGTAT 423
DB TTCAAGGTAATCTCTTGTGCTTAACCCAGTGTGACGTTTGTGACTTACTCAACTGG 1880

QY 424 AAGCGGTGAGGTTTCCATTAAGCAGATTATCGGCTCAGGTACAGTTCTGGATCTGCT 483
DB AAATCTCTGTTTCCCTAAAGAACGCTTATCGGTTTCAGGTACTTCACTTGACTCAGCT 1820

QY 484 CGTTTAAATACATCTCGAGAGACCTTCAAGATCTCATCGACAGCATCGATGCTGT 543
DB CGTTTCGCTCAAGCACTTGTCTGAAAATTTGGATGTGGATCTCGTTTCAGTGCACGCTAC 1760

QY 544 GTAATTGAGAACATGTTGTTGCGGTGTCGCTGCTGCTCTTACCAACATCGACGCG 603
DB ATCATGGGTGAACACGCTGACTCTGAGTTCGCTGTTTGGTTCACACGCTAACATCGCTGGT 1700

RESULT 4

US-09-166-350-31
; Sequence 31, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex

; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; FILE OF INVENTION: Uses Therefor
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-166-350-31

Query Match 12.9%; Score 125; DB 4; Length 1661;
Best Local Similarity 48.6%; Pred. No. 2.7e-30;
Matches 378; Conservative 0; Mismatches 390; Indels 9; Gaps 1;

QY 52 AAAGTTGTGCTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGCGTATACGTTGCTTCTC 111
DB AAGATTACAGTTGTTGGGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 220

QY 112 ACGGCATCGTTTCCGAGATTGTCTTATCGACGTGAACAAAGACAAAGACAGAGGTGAA 171
DB AAGGACTTGGCAGATGAACCTTGTCTTGTGTATGTCTGAAAGACAAATTTGAAGGGAGAG 280

QY 172 AGCATGGACTTAAACCCAGCAGCCTTCAATATACAGGTCTCGA-----GCGGTT 222
DB ATGATGGATCTCAACATGGCAGCCTTTTCCTTAGAACACCAAGATGTCTCTGGCAAA 340

QY 223 GATTATCTGACTGCGGCTGGCGGCCATGTTTATTTGTACATGTGGGATTAACCAAAAA 282
DB GACTATATGTAATGCAACTTCAAGCTGCTTATATCACGGCTGGGCACTGAGCAA 400

QY 283 AATGGACAAACAGGATGGATCTTGTCTGCAAAAAATGCCAACATTAATGCTGGAATCATC 342
DB AATGGACAAACAGGATGGATCTTGTCTGCAAAAAATGCCAACATTAATGCTGGAATCATC 342

Db 401 GAGGAGAAAGCCGCTCTTAATTTGGTCCAGGTAACGTAACATATTTAAATTCATCAT 460
 Qy 343 CCNATGTTGCCAAATATGCTCTGATACCATCTCTGTTATTTGCCAGCAATCTCTGAT 402
 Db 461 CCTAATGTTGTAATAACAGCCGCAACTGCAAGTTGCTTATTTGTTCCAAATCCAGTGAT 520
 Qy 403 GTTTTGACCTATATTTAGCTATAGCGGCTCAGGTTTCCACTAGCAGAGTTATCGGCTCA 462
 Db 521 ATCTTGACCTACGTTGGCTTGAAGATAGTGGTTTCCAAACCGTGTTATTTGGAGT 580
 Qy 463 GGTAAGTTCTGATATCTGCTGTTTAAATATCATCTCGGAGAGCACTTCAAGATCTCA 522
 Db 581 GGTGCAATCTGATTCAGCCGATTCGTTACCTGATGGGAAAGGCTGGGATTCAC 640
 Qy 523 TCGAGACATCGATGCTGTGTAATTTGGAGAACATGTTGCTGATTCGGGTGTCCTGCTGG 582
 Db 641 CCATTAAGCTGTCAATGGTGGTCTTTGGGGAACATGGAGATTCAGTGTGCTGTATGG 700
 Qy 583 TCTCTTACCAACATCGAGCGCATGAAGCTCGGATTTACTCGGAAAGCAACACATA 642
 Db 701 AGTGAATGAATGTTGCTGTGCTCTCTGAAGACTCTGCACCCAGATTTAGGACTGAT 760
 Qy 643 TTTGATCAGATGCTGTTCCATAGATCTTTGAGCAACGCGAGACGCTGCTTACGATATC 702
 Db 761 AAAGATAAGGAACAGTGGAAAGAGTTTCACAAGCAGGTGTTGAGAGTCTTATGAGGTG 820
 Qy 703 ATCAAGGCAAGGCTATCTTATGATGGAATCCAGCGGGATTTACTTCGCATAGTAAG 762
 Db 821 ATCAAGCTCAAGGCTACATCTCTGGGCTATTTGGACTCTCTGTAGCAGATTTGGCAGAG 880
 Qy 763 GCGATTTTAGAGGATACAGGATCCACATTTACAGTTTCAACCGTTGCTGATTTATTT 819
 Db 881 AGTATATGAAGATCTTAGCGGGTGCACCCAGTTTCCACCATGATTAAGGCTCT 937

RESULT 5

US-09-166-350-22
 ; Sequence 22, Application US/09166350A
 ; Patent No. 6440663
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Matthew
 ; APPLICANT: Chen, Yao
 ; APPLICANT: Stockert, Elisabeth
 ; APPLICANT: Old, Lloyd
 ; APPLICANT: Jager, Elke
 ; APPLICANT: Knuth, Alex
 ; TITLE OF INVENTION: Renal Cancer Associated Antigens and
 ; FILE REFERENCE: L0461/7051
 ; CURRENT FILING DATE: 1998-10-05
 ; EARLIER FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 1260
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-166-350-22

Query Match 11.3%; Score 109.8; DB 4; Length 1260;
 Best Local Similarity 47.7%; Pred. No. 1.9e-25;
 Matches 361; Conservative 0; Mismatches 387; Indels 9; Gaps 1;
 Qy 61 GTAGTGGAGTGGGAAGTTGGTCTGCCACAGCTATAGCTTCTTCAGCGGCATC 120
 Db 130 GTAGTGGTGTGGCAAGTTGGTATGCGGTGCTATCAGCACTTCTGGGAAAGTCTCTG 189
 Qy 121 GTTTCGAGATGCTTATCGAGTGNACAAAGCAAGCAGAGGGTGAAGCATGGAC 180
 Db 190 GCTGATGAACCTGCTCTTGTGGATGTTTGGAAAGATAAGCTTAAAGGAGAAATGATGAT 249

Qy 181 TTAACACCGC-----CAGCACCTTCAAAATACAAGTCTCGAGCGGGTGATTATCT 231
 Db 250 CTGCAGCATGGAGCTTATTTCTTTCAGACACCTAAAATTTGTGCAGATAAAGATTATCT 309
 Qy 232 GACTCGCTGGCGCGGCCATTGTTATTTGTCATGTTGGATTAAACCAAAAAATGGACAA 291
 Db 310 GTGACCGCCAAATCTTAAGATTGTAGTGGTAACTGCGAGGAGTCCGTGAGCAAGAGGGAG 369
 Qy 292 ACAGGATGGATCTTGCTCAAAAATGCCAACATTATCTCGAATCATCCCCATGTT 351
 Db 370 AGTCGCTCAATCTGCTGCGAGAGAAATGTTAATGCTTCAAAATCATTAATCTTCAGATC 429
 Qy 352 GCCAAATATGCTCTGATACCATCTCTTATTGCCAGCAATCTGCTCGATGTTTGAAC 411
 Db 430 GTCAGTACAGTCTGATGATGATCAATTTGTTTCCAAACCCAGTGCACATTCTTACG 489
 Qy 412 TATATTAGCTATAAGCGCTCAGGGTTTCCATTAAGCAGAGTTATCGGCTCAGTACAGTT 471
 Db 490 TATGTTACCTGGAACATAAGTGGATTACCCAAACACCGCGTGAATGGAAGTGGATGAAT 549
 Qy 472 CTGGATACCTGCTGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCATCGGACAGC 531
 Db 550 CTGGATTTCTGATGATTTTCGCTACCTTATGGCTGAAAAAATTTGGCAATCATCCAGCAGC 609
 Qy 532 ATCGATGCTGTGTAATTCGAGAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
 Db 610 TGGCATGATGATGATTTTGGGGGAAACATGGGACTCAAGTGTGCTGTGTTGGAGTGTG 669
 Qy 592 AACATCGACGGCATGAAGCTCCGGGATTAATCGGAAAAAGCAACCAATATTTGATCAG 651
 Db 670 AATGTGCGAGGTGTTCTCTCCAGGAATTTGAATCCAGAAATGGAACTGCAATGATAGT 729
 Qy 652 AATGCTTCCATAGATCTTTGAGCAACCGGAGCGCTTACGATATCATCAAGCGC 711
 Db 730 GAAATTTGAAGGAAGTGCATAAGTGGTGGTGAAGTGGCTATGAAGTCAATCAAGCTA 789
 Qy 712 AAAGCTTACTTTCATATGGAATCGAGCGGGATTAATCTTCGCATAGTAAGCGGATTTTA 771
 Db 790 AAAGGATATACCAACTGGGCTATTTGATTAAGTGTGCTGATCTTATTGAATCCTATGTTG 849
 Qy 772 GAGGATACAGGATCCACATTACAGTTTCAACGGTTG 808
 Db 850 AAAATCTATCCAGGATTCATCCGTGTCAACAATGG 886

RESULT 6

US-08-869-506-1
 ; Sequence 1, Application US/08869506
 ; Patent No. 5827710
 ; GENERAL INFORMATION:
 ; APPLICANT: Uchida, Kohji
 ; APPLICANT: Matsukawa, Hirokazu
 ; APPLICANT: Matuo, Yushi
 ; APPLICANT: Fujita, Teyosi
 ; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
 ; LACTATE DEHYDROGENASE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 5827710th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/869,506
 ; FILING DATE: 05-JUN-1997
 ; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 73797/1996
 ; FILING DATE: 29-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 159-43
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1240 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 55..1053
 ; US-08-869-506-1

Query Match 10.4%; Score 101.2; DB 1; Length 1240;
 Best Local Similarity 50.2%; Pred. No. 1.1e-22;
 Matches 284; Conservative 0; Mismatches 273; Indels 9; Gaps 1;

QY	61	GTAGTCGGAGTGGGAAGTGTGGGTCTGCCACAGCGTATACGTTGCTTCTCAGCGGCATC	120
Db	127	GTGGTGGGGTGGCGAGGTGGGATGGCGTATCAGCATCAGCATCTCGGCAAGGTCTT	186
QY	121	GTTCGCGAGTGTCTTATCGACGTGAACAAGACAAGACGAGGTGAAGAGCATGGAC	180
Db	187	TGTGATGAGCTTGTCTGTGTTGATGTTTGAAGACAAGCTAAAGAGGAATGATGAT	246
QY	181	TTAAACACAG-----CAGCACCTTCAATACAGGTCTCGAGCGGTGATTCCT	231
Db	247	CTACAGCATGGCAGCTTGTTCCTTCAGACTCATAAGATTGTGGCAGACAAGATTATGCT	306
QY	232	GACTGCGTGGCGGCCATTTGTTATGTCACATGTGGATTACCAAAAATCGACAA	291
Db	307	GTCACAGCCAACTCCAAGATTGGTAGTAACCTCAGGTGTTCGTCAGCAAGAGGGGAG	366
QY	292	ACAAGGATGGATCTTGTCTGCAAAAATGCAATTCCTCGAGAGCACTTCAAGATCTCAT	351
Db	367	AGTGTCTCAACCTGGTTCAGAGGATGTGAACGCTTCAAAATCATCATCTCCTCAGATT	426
QY	352	GCCAAATATGCTCTGTATACCATCTCTGTATATGCCAGAAATCTCTGATGTTTGGAC	411
Db	427	GTGAAATACAGCCCAATTCGACTATCTCTGTGGTTTCCAAACCCAGTGGATATTAACC	486

RESULT 7

US-09-128-967-1
 ; Sequence 1, Application US/09128967
 ; Patent No. 6057141
 ; GENERAL INFORMATION:
 ; APPLICANT: Uchida, Kohji

; APPLICANT: Matsukawa, Hirokazu
 ; APPLICANT: Matuo, Yushi
 ; APPLICANT: Fujita, Tutosi
 ; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
 ; NUMBER OF INVENTION: LACTATE DEHYDROGENASE
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 6057141th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/128,967
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/869,506
 ; FILING DATE: 05-JUN-1997
 ; APPLICATION NUMBER: JP 73797/1996
 ; FILING DATE: 29-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 159-43
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1240 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 55..1053
 ; US-09-128-967-1

Query Match 10.4%; Score 101.2; DB 3; Length 1240;
 Best Local Similarity 50.2%; Pred. No. 1.1e-22;
 Matches 284; Conservative 0; Mismatches 273; Indels 9; Gaps 1;

QY	61	GTAGTCGGAGTGGGAAGTGTGGGTCTGCCACAGGTATACGTTGCTTCTCAGCGGCATC	120
Db	127	GTGGTGGGGTGGCGAGGTGGGATGGCGTATCAGCATCCTCGGCAAGGTCTT	186
QY	121	GTTCGCGAGTGTCTTATCGACGTGAACAAGACAAGACGAGGTGAAGAGCATGGAC	180
Db	187	TGTGATGAGCTTGTCTGTGTTGATGTTTGAAGACAAGCTAAAGAGGAATGATGAT	246
QY	181	TTAAACACAG-----CAGCACCTTCAAAATACAGGTCTCGAGCGGTGATTCCT	231
Db	247	CTACAGCATGGCAGCTTGTTCCTTCAGACTCATAAGATTGTGGCAGACAAGATTATGCT	306
QY	232	GACTGCGTGGCGGCCATTTGTTATGTCACATGTGGATTACCAAAAATCGACAA	291
Db	307	GTCACAGCCAACTCCAAGATTGGTAGTAACCTCAGGTGTTCGTCAGCAAGAGGGGAG	366
QY	292	ACAAGGATGGATCTTGTCTGCAAAAATGCCAAATATGCTGGAAATCATCCCCAATGTT	351
Db	367	AGTGTCTCAACCTGGTTCAGAGGATGTGAACGCTTCAAAATCATCATCTCCTCAGATT	426
QY	352	GCCAAATATGCTCTGTATACCATCTCTGTATATGCCAGAAATCTCTGATGTTTGGAC	411
Db	427	GTGAAATACAGCCCAATTCGACTATCTCTGTGGTTTCCAAACCCAGTGGATATTAACC	486

QY 412 TATATTAGCTATATAGGGCTCAGGGTTTCCACTAAGCAGAGTATTCGGCTCAGGTACAGTT 471
Db 487 TATGTACATGGAAGCTGAGTGGCTGCCAAAGCACCCTGTGATTTGGAAGTGGCTGCAAT 546
QY 472 CTGATATCTGCTCGCTTTTAAATACATCCTCGGAGAGCAGCTTCAAGATCTCATCGGACAGC 531
Db 547 CTAGACACAGTAACTTCGGCTACTGATGCTGAGAGACTTGGTATCCACCCCAACAGC 606
QY 532 ATCGATGCTGTGTAATGAGAGACATGGGTGATTCGGGTGCTGCTGCTCTCTTACC 591
Db 607 TGCATGCTGATTTAGGAGAACATGGTGAATCTAGTGTGGCTGTTGGAGCGGAGTT 666
QY 592 AACATCGACGCGATCAAGCTCCGGGA 617
Db 667 AATGTGTAGGTGTTCTCTCCAGGA 692

RESULT 8
US-09-535-381-1
; Sequence 1, Application US/09535381
; Patent No. 6268189
; GENERAL INFORMATION:
; APPLICANT: Skory, Christopher D
; TITLE OF INVENTION: Fungal Lactate Dehydrogenase Gene and Constructs for
; TITLE OF INVENTION: the Expression Thereof
; FILE REFERENCE: Dkt 0110.98 - Christopher D. Skory
; CURRENT APPLICATION NUMBER: US/09/535,381
; CURRENT FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Rhizopus oryzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)..(994)
US-09-535-381-1

Query Match 9.7%; Score 93.8; DB 4; Length 1116;
Best Local Similarity 47.5%; Pred. No. 2.6e-20;
Matches 429; Conservative 0; Mismatches 447; Indels 27; Gaps 4;
QY 51 AAAAGTTGTGTAGTGGAGTGGAGTGTGGCTCTGCCACAGCGTATACGTTGCTTCT 110
Db 46 AAAGTGTGCTATGCTGGAGTGTGGAGTGTGGCTCTGCCACAGCGTATACGTTGCTTCT 105
QY 111 CAGCGGATCGTTTCCGAGATTTCTTATCGAGTGAACAAAGCAGAGGCTGA 170
Db 106 TAAACAATTTGTACAGAAATCATTTTGTATGTTTATCTGACATCGTTCAAGCTCA 165
QY 171 AAGCATGAGCTTAAACACGAGCAGCCTTCAATACAAAGTTC---TCGAGCGGTGATTA 227
Db 166 AGTCTTGACCTTGCAGATGCTGCGAGTATAAGTCAACAGCCCATCGAGCAGGTAGCGC 225
QY 228 TCCTGACTGCTGGCGGCGCATTTTATGTCATGTTGGGATTAACCAAAAATGG 287
Db 226 AGAGGAGCGCAGGCGAGCAGATTTTGTTCATCAGCGCGGTGCGAAACAAAGGGAAG 285
QY 288 ACAACAGAGGATGATCTTGTGCAAAAATGCAACATTTATGCTGGAATCATCCCAA 347
Db 286 TGAGCCTCGGACAAGCTCATTTGAACGAATCTCAGAGTGTGCAAGATATCATGTTGG 345
QY 348 TGTGCAAAATPATGCTCCTGATACCATCTGCTTATTTGCCAGGAATCCTGTCGATGTTT 407
Db 346 CATGCAACCCATTCGACAGCAGCAGTCACTTGTGGTGTAGCAATCCAGTCGATATCTT 405
QY 408 GACCTATATTAGCTATAAGGGCTCAGGTTTCCACTAAGCAGAGTATTCGGCTCAGGTAC 467
Db 406 GACACATTTGCAAGACCCCTCTCTGCACTGCTCCAAACCAAGGTCAATGGCTCCGCTAC 465
QY 468 AGTTCTGATACTGCTCGTTTTTAAATACATCTCTCGGAGAGCACTTCAAGATCTCATCGGA 527

Db 466 CTACCTTGACAGCAGCCGCTTCGGCGTCATCTTGGGATGCTTTTGATGTCAATCTCA 525
QY 528 CAGCATCGATGCTGTGTAATTTGGAGAACATGGTGAATTCGGGTGTCCTGTCTGTGCTCT 587
Db 526 ATCGGTCCATGCTTTTGTCTTGGGTGAACATGGGATTCGCCAGATGATCGCTTGGGAGGC 585
QY 588 TACCAACATCGAGCGCATGAAGCTCCGGGATTTACTGCGRAAAGCCCAACACATATTTGA 647
Db 586 TGCCTTCGATTTGGTGGCCAGCCGTTGCAAGTTTCCCGGAATTCGCAAGC-----TGGAT 640
QY 648 TCAGATGCTGTTCCATAGAAATCTTTGAGCAAAAGCGGAGACGCTGCTTACGATATCATCA 707
Db 641 AAAACAGCAATTTCAAAGCGATATCAGGTAAGCGA-----TGGAGATCAATTCG 690
QY 708 GGCAGAGCTATATCTTCAATATGGAATCGCAGCGGATTTACTTCGATATGTAAGGCGAT 767
Db 691 TTTGAAAGGAGCCACGTTTTTATGGAATTTGTCGCTGTCAGCGGATTTAGTGCACACTAT 750
QY 768 TTTAGAGGATACAGGATCCACACTTACAGTTTCAACCGTTGGTGATTTATTTGGGGTTGA 827
Db 751 CATGTTGAATAGGAATCAGTATCAGTCCAGTTTC-----TGTTATGTTGAAAAGTA 801
QY 828 ACAAAATTGCTATAAGCGCTCCCTACCAAACTCAATAAAAGTGGGCTCATCAAGTGGCTGA 887
Db 802 TGGAGCCACTTTTCTATGCTCTGCTTAACTTGGATGGAGAGGTGTTGAACAGATCTATGA 861
QY 888 ACTTTCACATCGATGAGAGGAATAGATTTGATGGAATAATCAGCTAGTCAGATCAATC 947
Db 862 AGTACCCTGACGGAAGAAGACGCTTGTCTGTGTAATCTGTAGAGGCATTTGAAATC 921
QY 948 AGT 950
Db 922 AGT 924

RESULT 9
US-09-535-381-3
; Sequence 3, Application US/09535381
; Patent No. 6268189
; GENERAL INFORMATION:
; APPLICANT: Skory, Christopher D
; TITLE OF INVENTION: Fungal Lactate Dehydrogenase Gene and Constructs for
; TITLE OF INVENTION: the Expression Thereof
; FILE REFERENCE: Dkt 0110.98 - Christopher D. Skory
; CURRENT APPLICATION NUMBER: US/09/535,381
; CURRENT FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6072
; TYPE: DNA
; ORGANISM: Rhizopus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3100)..(4062)
US-09-535-381-3

Query Match 9.7%; Score 93.8; DB 4; Length 6072;
Best Local Similarity 47.5%; Pred. No. 6.5e-20;
Matches 429; Conservative 0; Mismatches 447; Indels 27; Gaps 4;
QY 51 AAAAGTTGTGTAGTGGAGTGGAGTGTGGTCTGCCACAGCGTATACGTTGCTTCT 110
Db 3114 AAAGTGTGCGCATCGTTGGAGCTGGTGCAGTAGAGCCTCCACTGCTTATGCACTTATGTT 3173
QY 111 CAGCGGATCGTTTCCGAGATTTGCTTATCGAGTGAACAAAGCAGAGGAGGTGA 170
Db 3174 TAAACAATTTGTACAGAAATCATTTATGTTGATGTTATCTGACATCGTTCAAGCTCA 3233
QY 171 AAGCATGGAATTAACACGAGCAGCTTCAATACAAAGTTC---TCGAGCGGGTGATTA 227
Db 3234 AGTCTTGAACCTTGAGATGCTGCCAGTATAGTACAGGCCCATCCGAGCAGGTAGCGC 3293

CORRESPONDENCE ADDRESS:
ADDRESSEE: Levdig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,418
FILING DATE: 17-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Allen E.
REGISTRATION NUMBER: 37354
REFERENCE/DOCKET NUMBER: 78339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (25)3533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Bacillus stearothermophilus*
STRAIN: ATCC12016
US-08-838-418-1

Query Match 9.2%; Score 89.2; DB 1; Length 1912;
Best Local Similarity 51.8%; Pred. No. 1.1e-18;
Matches 202; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 223 GATTATCTGCTGCTGGCGGCCATTGTTATGTCACATGTTGGATTAAACCAAAAA 282
DB 887 GATTACGCTGACAGCGGATCCGACATCGTCTCATCAGCAGGATCGCCGCGAAG 946
QY 283 AATGACAAAACAAGATGATCTTGTCTGCAAAAAATGCAACATTATGCTGGAATCATC 342
DB 947 CCGGSGATGACCGCGAGATTGTTGTGACGACGACCAAAAAATATGAAGCAAGTGCAG 1006
QY 343 CCCAATGTTGCCAATATGCTCTGTGATACCATCTGCTTATGTCACGAAATCTCTGTGAT 402
DB 1007 AAGGAAGTCGTCAAAATACTCGCCGAACTGCTACATCATCTGCTTTGACGAAACCCGCTCGAT 1066
QY 403 GTTTTGACCTATATTAGCTATAAGCGCTCAGGTTTCCACTAAGCAGAGTTATCGGCTCA 462
DB 1067 GCGATGAGTATACGGTCTTTTAAGATTCGGATTCGGAATAACCGGCTCATCGGCGAG 1126
QY 463 GGTACAGTCTCGGATCTGCTCGTTTTAAATACATCTCTCGGAGACACTTCAAGATCTCA 522
DB 1127 TCGGCGCTTTGGATACGCGCGCTTCGCGACGTTCTGTCGCGAGGAGCTGAACATTTG 1186
QY 523 TCGGACAGCATGATCCCTGTGTAATTGGAGAAATGTTGATTCGGGTGTCCTGTCTGG 582
DB 1187 GTAAAGATGTCACTGGGTTTGTGTTAGGCGGCCATGCGCATGACATGGTGCCTCTGTC 1246

QY 583 TCTCTTACCACATCGACGGCATGAAGCTC 612
DB 1247 CGCTACTCGTACGCCGGCGCATTCGCTC 1276

RESULT 12
US-09-134-001C-2696
; Sequence 2696, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2696
; LENGTH: 978
; TYPE: DNA
; ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-2696

Query Match 8.3%; Score 81; DB 4; Length 978;
Best Local Similarity 51.5%; Pred. No. 3.3e-16;
Matches 186; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 245 CGGCCATTCTTATGTCACATGTTGGATTAAACCAAAAAATGCAAAACAAAGGATCGATC 304
DB 260 CAGACATAGTGGTATGACTGCGAGGTATACCTAGGAAATCAGGAATGACAGAGAAGAT 319
QY 305 TTGCTGCAAAAAATGCAACATTATGCTGGAATCATCCCAATGTTGCCAAATATGCTC 364
DB 320 TAGTTCAAACTAATGAACAATAGTACGAGAACTGCATTACAAATTCGCAACGTATGCAC 379
QY 365 CTGATACCATCTGCTTATGTCACGAAATCTGTCGATGCTTTTGACCTATATAGCTATA 424
DB 380 CTCAATCAATAATATTGTTATGACTAAATCCGTTGATGATGATGATGATGATGATGAT 439
QY 425 AGCGCTCAGGTTTCCACTAAGCAGAGTTATCGGCTCAGTCACTGCTGCTGCTGCTGCTC 484
DB 440 AAGCATCAGTTTCTTAAAGAACGTATTATGTTGCTCAATCTGGAATTTAGAGCTGCAA 499
QY 485 GTTTTAAATACATCTCTCGGAGAGCACTTCAAGATCTCATCGGACAGCATGATGCTGTG 544
DB 500 GATATCGAACTTTTATTGCTCAAGAACTTAAACGTTCTGTCAAAGATGTAATGGGTTG 559
QY 545 TAATTGGAGAACATGTTGATTCGGGTGTCGCTGCTGCTGCTCTTACCAACATCGACGGCA 604
DB 560 TTTTAGTGGACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
QY 605 T 605
DB 620 T 620

RESULT 13
US-09-328-111-455
; Sequence 455, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endegre, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan

APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 455
LENGTH: 566
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(566)
OTHER INFORMATION: n = A, T, C or G
US-09-328-111-455

Query Match 8.2%; Score 79.8; DB 4; Length 566;
Best Local Similarity 48.4%; Pred. No. 5.9e-16;
Matches 216; Conservative 0; Mismatches 230; Indels 0; Gaps 0;
QY 363 TCCTGATACCATCTGCTTATTCGCCAGCATCTGTCGATGTTTTCACCTATATTAGCTA 422
Db 5 TCTGATTCGATCATATATTTGTTGTTCCAAACCAGTGGACATTTCTACGTATGTTACCTG 64
QY 423 TAAGGCTCAGGTTTCCACTAAGCAGAGATTATCGGCTCAGGTACAGTTCTCGATACCTGC 482
Db 65 GAAACTAAGTGGATTACCCAAACACCGCGTATTGGAAGTGGATGTAATCTGGATTCGC 124
QY 483 TCGTTTAAATACATCTCGGAGAGACATTCAGATCTCATCGGACAGATCGATCGCTG 542
Db 125 TAGATTTCGCTACCTTATGCTGCTGAAACACTTGGCAATTCATCCAGCAGCTGCCATGGATG 184
QY 543 TGTAAATTGGAGAACATGCTGATTTCGGGTGTCGCTGCTGCTCTCTTACCAACATCGACGG 602
Db 185 GATTTTGGGGAAACATGGCGACTCAAGTGTGGCTGTGTGGAGTGGTGTGATGTGGCAGG 244
QY 603 CATGAAGCTCCGGGATTTACTCGGAAAGCAACACCATATATTTGATCAGAAATCGGTTCCA 662
Db 245 TGTTTCTCTCCAGGAATTGAATCCAGAAATGGGAATCGACAATGATGAGAAATGGAA 304
QY 663 TAGAATCTTGAGCAACGCGACAGCGTCTTACGATATCATCAAGCGCAAGGCTATAC 722
Db 305 GGAAGTGCATAAGATGGTGTGTTGAAAGTGCCTATGAAGTCTCAAGCTAAAGGATATAC 364
QY 723 TTCATATGGAATCGACGCGGATTACTTCGCATAGTAAAGGCGATTTTAGAGGATACAGG 782
Db 365 CAACTGGGCTATTGGATTAAAGTGTGGCTGATCTATTGAATCATGNTGAAAAATCTATC 424
QY 783 ATCCACATTTACGATTTTCAACCGTTG 808
Db 425 CAGGATTCATCCCGNGTCAACNATGG 450

RESULT 14
US-08-920-812-7
Sequence 7, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5024 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORGANISM: Staphylococcus epidermidis
ORIGINAL SOURCE:
SPRAIN: Clinical isolate SE-32
US-08-920-812-7

Query Match 7.6%; Score 74.2; DB 1; Length 5024;
Best Local Similarity 51.7%; Pred. No. 1.2e-13;
Matches 169; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 279 AAAAAATGACAAACAGGATGGATCTTCTCGAAAAAATGCCAACATTATGCTGGAAT 338
Db 306 AAATCAGGAATGACAGGAGAGAAATAGTTCAAACTAATGAACAAATAGTACGAGAAC 365
QY 339 CATCCCAATGTTGCCAAATATGCTCTGATACCATCTTATTCGCCAGCAATCCTGT 398
Db 366 TGCATTACAAATGCAACGATGACCTCATTCAAATAATATTGATTGACTAATCCGGT 425
QY 399 CGATGTTTTGACCTATATTAGCTATAAGGCGTCAGGGTTTCCACTAAGCAGAGTTATCGG 458
Db 426 TGATGTTATGACATATATCTGCAATTTAAAGCATCAGGTTTTCTTAAAGACGTTATTGG 485
QY 459 CTCAGGTACAGTTCTGGATCTGCTGTTTAAATACATCTCCGGAGAGACCTTCAAGAT 518
Db 486 TCAATCTGGAATTTTAGACGCTCAAGATATCGAACTTTTATTGCTCAAGAACTTAACGT 545
QY 519 CTCATCGGACAGCATCGCTGCTGTTAATTCGAGAACATGGTGTATTCGGGTGCTGCTGT 578
Db 546 GTCTGTCAAGATGTAATAGGGTTTGTGTTTAGTGACATGTTGATACGATGTACCTTT 605
QY 579 CTGGTCTCTTACCAACATCGACGGCAT 605
Db 606 GATTAATAACACACACATTAAATGGAT 632

RESULT 15
US-08-920-827-7
Sequence 7, Application US/08920827
Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio

Job time : 65 secs

APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5024 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-32
US-08-920-827-7

Query Match 7.6%; Score 74.2; DB 1; Length 5024;
Best Local Similarity 51.7%; Pred. No. 1.2e-13;
Matches 169; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy	279	AAAAAATGGACAAACAAAGGATGATCTTGTGCAAAAAATGCCAACATTATGCTGGAAT	338
Db	306	AAATCAGGATGACAGAGAGAGAGATTAGTTCAAACTAATGACAAATAGTACGAGAAC	365
Qy	339	CATCCCAATGTTGCCAAATATGCTCTGTATACCATCTGCTTATTCGCCAGAACTCTGT	398
Db	366	TGCATTACAAATGCAACGATGACACCTCATTCATAATATTGTTATGCTAATCCGGT	425
Qy	399	CGATGTTTTCACCTATATAGCTATAGGCTCAGGGTTCCACTRAGCAGAGTTATCGG	458
Db	426	TGATGTTATGACATATCTGCAITTAAGCATCAGGTTTTCCTAAGAACGTTATTGG	485
Qy	459	CTCAGGTACAGTCTCGGATCTCGTCTTTTAAATACATCTCGGAGAGCACTTCAAGAT	518
Db	486	TCAATCTGGAATTTAGACGCTGCAAGATATCGAATTTATTGCTCAAGACTTAACGT	545
Qy	519	CTCATCGACAGATCGATGCTGTGTAAATGGAGAACATGGTGATTCGGGTGTCCTGT	578
Db	546	GTCTGTCAAGATGTAATGGGTTTGTGTTAGGTGGACATGGTGATGTTACCTTT	605
Qy	579	CTGGTCTCTTACCAACATCGACGGCAT	605
Db	606	GATTAATAACACACACATTAATGGAT	632

Search completed: July 31, 2003, 11:02:32

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 09:47:41 ; Search time 260 Seconds
(without alignments)

7712.449 Million cell updates/sec

Title: US-09-992-430B-21

Perfect score: 972

Sequence: 1 atgttcaagatacaaaagtc.....ttgagcatctggagatcaat 972

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186.2	19.2	28690	11	US-09-070-927A-138
2	183.6	18.9	1255	10	US-09-971-361-2
3	173	17.8	13154	11	US-09-070-927A-338
4	172.6	17.8	3264	8	US-08-781-986A-424
5	159.8	16.4	14333	8	US-08-781-986A-57
6	154.2	15.9	942	11	US-09-738-626-3210
7	154.2	15.9	3309400	11	US-09-738-626-1
8	151	15.5	747	11	US-09-974-300-73
9	136	14.0	1146	15	US-10-274-266-1
10	136	14.0	1759	11	US-09-731-872-14
11	136	14.0	3144	15	US-10-274-266-3
12	123.6	12.7	1062	11	US-09-938-842A-1938
13	121.2	12.5	4913	10	US-09-971-361-1
14	120.8	12.4	1755	11	US-09-731-872-15
15	109.8	11.3	1172	11	US-09-974-298-74
16	109.8	11.3	1272	15	US-10-177-293-261

17	109.8	11.3	2719	15	US-10-198-846-11544	Sequence 11544, A
18	109.8	11.3	3397	15	US-10-198-846-11555	Sequence 11555, A
19	108.2	11.1	2719	15	US-10-198-846-11544	Sequence 11544, A
C	106.4	10.9	491	11	US-09-960-352-9428	Sequence 9428, Ap
20	106.4	10.9	734	10	US-09-910-943-711	Sequence 711, Appl
21	102.2	10.5	1362	11	US-09-974-298-73	Sequence 73, Appl
22	102	10.5	1362	15	US-10-044-090-556	Sequence 556, Appl
23	102	10.5	1362	15	US-10-071-765-89	Sequence 89, Appl
24	102	10.5	1362	15	US-09-998-598-1409	Sequence 1409, Ap
25	100.6	10.3	496	11	US-09-998-598-1410	Sequence 1410, Ap
26	100.6	10.3	519	11	US-09-974-300-56	Sequence 56, Appl
27	85	8.7	822	11	US-10-198-846-2972	Sequence 2972, Ap
28	83.2	8.6	839	15	US-10-198-846-8917	Sequence 8917, Ap
29	83.2	8.6	883	15	US-10-198-846-8917	Sequence 455, Ap
30	79.8	8.2	566	11	US-09-879-536-455	Sequence 2988, Ap
31	76	7.8	891	15	US-10-198-846-2988	Sequence 1465, A
32	74.2	7.6	379	11	US-09-960-352-14665	Sequence 9276, Ap
33	72.6	7.5	974	15	US-10-198-846-9276	Sequence 1812, Ap
C	70.2	7.2	520	11	US-09-998-598-1812	Sequence 8905, Ap
C	70.2	7.2	893	15	US-10-198-846-8905	Sequence 773, Ap
35	69.2	7.1	530	11	US-09-833-381-773	Sequence 7674, Ap
36	66.4	6.8	394	11	US-09-960-352-7674	Sequence 1076, Ap
C	66.4	6.8	436	11	US-09-736-457-1076	Sequence 1076, Ap
C	66.4	6.8	436	11	US-09-902-941-1076	Sequence 1076, Ap
C	66.4	6.8	436	11	US-09-849-626-1076	Sequence 1076, Ap
C	66.4	6.8	436	15	US-10-017-754-1076	Sequence 1013, Ap
42	63	6.5	422	11	US-09-920-300A-1013	Sequence 1013, Ap
43	63	6.5	422	15	US-10-033-528-1013	Sequence 160, App
C	62.2	6.4	519	10	US-09-604-287A-160	Sequence 160, App
C	62.2	6.4	519	11	US-09-339-338-160	Sequence 160, App

ALIGNMENTS

RESULT 1

US-09-070-927A-138
Sequence 138, Application US/09070927A
Patent No. US20020120116A1

GENERAL INFORMATION:

APPLICANT: Charles A. Kunsch

Steven Barash

TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 982

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070, 927A

FILING DATE: 04-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046, 655

FILING DATE: 1997-05-16

APPLICATION NUMBER: 60/044, 031

FILING DATE: 1997-05-06

APPLICATION NUMBER: 60/066, 009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB369

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

Matches	481; Conservative	1; Mismatches	439; Indels	19; Gaps	4;
Qy	28	GTAAAGAACTGATGCCAAAAACAGTAAAGTTGTGGTAGTGGGAGTGGGAAGTGTGGGTCT	87		
Db	13342	GTAATGAACAAATTTAAAGGGAACAAAGTTGTATTAAATAGGTAATGGTGCAGTAGATTCA	13283		
Qy	88	GCACACAGGTATACGTTGCTTCTCAGCGGACGTGTTTCCGAGATTGTCTTATCGACGTG	147		
Db	13282	AGCTACGCATTTTCATTAGTAGAACCAAGCAATGTTGATGAATTAGTCATCATTTGATTTA	13223		
Qy	148	AACAAAGACAAACGACAGGAGTGAAGCATGGAGCTTAAACCGACGACGACCTTCAAAATACA	207		
Db	13222	GACACTGAAGAGTTCGAGAGATGTTATGGATTTAAACATGCCACACCATATTTCTCCA	13163		
Qy	208	AGGCTCTCG-----AGCGGGTGATTATCTCGACTGCGCTGGCGCGGCCCATTTGTTATT	258		
Db	13162	ACAACAGTTCTGTGTAAGAGCTGGCGAATACAGTGAATGTCATGATCGGATCTAGTTGTC	13103		
Qy	259	GTCCATGTGGGATTAAACAAAAAATGACAAAAACGAGATCGATCTTGTCTGCAAAAAAT	318		
Db	13102	ATCTGTGCTGGTGCTGCACAAAAACCTCGAGAAACACGTTTAGATTAGTATCTAAAAAC	13043		
Qy	319	GCCAAACATTATGCTGGAATCATCCCCAATGTGCCCATAATGCTCCTGTATACCATCTGTG	378		
Db	13042	TTGAAATATTCAAATCAATGTTGGTGAAGTAAATGGCATCAAAATTTGATGGTATTTTC	12983		
Qy	379	CTTATTTGCCACGAATCCTGTTCGATGTTTTGACCTATATTAGCTATAAGCGCGTCAGGGTTT	438		
Db	12982	TTGGTAGCTACAAATCCTGTGTGATATTTTAGCGTATGCAACATGAAATTTCTCTGTTTA	12923		
Qy	439	CCACTAAGCAGAGTTATCGGCTCAGGTACAGTCTCGGATCTGCTGCTTTTAAATACATC	498		
Db	12922	CCTAAAGAACGTTTATAGGTTCTGGTGACAAATTTTAGACTCTGCAACGCTTTAGATTATTG	12863		
Qy	499	CTCGGAGAGCACATTCAAGATCTCATCGGACAGCATCGATGCGTGTGAATTTGGAGAACAT	558		
Db	12862	TTAAGCGARC- GTNCGATGTTGGCCACGACGTAGCGTCAATTAATTTGGTGAACAT	12804		
Qy	559	GGTGATTCGGGTGTCCTGTCTGTCCTTTACCAATCGACGGCATGAAGCTCCGGAT	618		
Db	12803	GGTGACACTGAATTAACAGTATGGTCACACGCTAATATTGCGGTCACCTTTGAAGACA	12744		
Qy	619	TACTGCGAAAAGCCCAACACATATTTGATCAGATGCGTTCCTCATAGAACTTTTGACAA	678		
Db	12743	TTACTTTGAACAACGTCCTCAGGCGAAAGCGCAAAATTG-----AACAATAATTTTGTCTCAA	12690		
Qy	679	ACGCGAGACGCTGCTTACGATATCATCAAGCGCAAGGCTATACTTTCATATGGAATCGCA	738		
Db	12689	ACACGTGATGCAGCATATGACATTTTCAAGCTAAAGTGCCACCTATTATTTGGTGTGCA	12630		
Qy	739	CGCGGATTACTTCGCATAGTAAGGCGATTTTAGAGGATACAGGATCCACACTTACAGTT	798		
Db	12629	ATGGGATTAGCTAGATAATTACTGAAGCGATTTTCAGAAATGAAGATGCCGTATTGACTGTA	12570		
Qy	799	TCAAC---CGTTGGTGATTATTTTGGGGTTGAACAAATTTGCTATAGCGTCCCTACCAA	855		
Db	12569	TCAGCATTTATGAAGCGCAATATAGGAAGAAGATGTTTATTATTTGGTGTCCACAGTC	12510		
Qy	856	CTCAATAAAAAGTGGGCTCATCAAGTGGCTGAACCTTTCACTCGATGAGAAGGAATAGAA	915		
Db	12509	ATCAATAGAAACGGTATTTCGCAACGTCGTAGAAATCCCATTAACGACGACGAACAAGC	12450		
Qy	916	TTGATCGAAAAATCAGCTAGTCAGATCAAAATCAGTGAATTG	955		
Db	12449	AGGTTGCGCATTTTCAGCTAAAAACATTAAGAAATATTATATGG	12410		

RESULT 6

RES001 8
US-09-738-626-3210
; Sequence 3210, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI

```

; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3210
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3210

Query Match      15.9%: Score 154.2; DB 11; Length 942;
Best Local Similarity 50.8%; Pred. No. 4.2e-36;
Matches 456; Conservative 0; Mismatches 423; Indels 18; Gaps 3;

Qy 52 AAAGTTTGTTGTTAGTGGAGTGGGAAGTGTGGGGTCTGCCACAGCGTATACGTTGCTTCTC 111
Db      |||||
Qy 112 AGCGGCAATGTTCCCGAGATTGCTCTATCGACGTGAACAAAGACAGAGAGGGTGA 171
Db      |||||
Qy 82 CAGGGCATGCGAGATCATCTTGGCATCATCGACATCGATGAAAAGAACTCGAAGGCAAC 141
Db      |||||
Qy 172 AGCATGACATTAACCAACGCA-----GCACCTTCAAAATCAAGGTCTCGAGCGGGT 222
Db      |||||
Qy 142 GTCATGACATTAACCAATGTTGTTGTGGGCGGATTTCCGCGACCCCGGTCCACCAAGGGC 201
Db      |||||
Qy 223 GATTATCTGACTGCGTGGCGGGCCATTTGTTATTGTCTCATGTGGGATTAACCAAAA 282
Db      |||||
Qy 202 ACCTACGCTGACTGCGAAGACGCGACCATGTTGTCATTTGTGCGGCGCAGCCCAAAG 261
Db      |||||
Qy 283 AATGGAACAACAGGATGATCTTTGCTGCAAAAATAATGCCAACTATATGCTGGAATCATC 342
Db      |||||
Qy 262 CCAGGCGAGACCGCGCTCCAGCTGGTGGACAAAAACGTCAAGATTATGAAATCCATCGTC 321
Db      |||||
Qy 343 CCCAATGTTGCCAAATATGCTCTGTATACCATCTGCTTATTCGCAAGATCTCTGTGAT 402
Db      |||||
Qy 322 GCGGATGTCATGACAGCGGATTCGAGCGCATCTTCTCTGTGGCGTCCAAACCGAGTGGAT 381
Db      |||||
Qy 403 GTTTTGACCTATATTAGCTATAAGGCGTCAAGGTTTCCACTAAGCAGAGTATCGGCTCA 462
Db      |||||
Qy 382 ATCTGACCTACGCGAGTGGAAATTTCCGGCTTGGAAATGGAAACCGGTGATCGGCTCC 441
Db      |||||
Qy 463 GGTAAGTCTTGGAATCTGCTCGTTTTAAATACTCTCGGAGAGCACTTCAAGATCTCA 522
Db      |||||
Qy 442 GGAATGTCCTGGAATCTCGCTCGATTCCGCTCATATGCTGGGCGAACTCTACGAAGTGCA 501
Db      |||||
Qy 523 TCGGACAGCATCGATGCTGTGTAATTTGGAGAACATGGTATTCGGGTGTGCTGTCTGG 582
Db      |||||
Qy 502 CCAAGCTCCGTCACGCGCTACATCATCGGCGAACACGCGGACACTGAACTTCCAGTCTTG 561
Db      |||||
Qy 583 TCTCTTACCAACATCGAGCGCATGAAGCTCCGGGATTTACTCGGAAAAGCAACACATA 642
Db      |||||
Qy 562 TCCTCCGCGACCATTCGACGCGGTATCGCTTAGCGGAATGCTGGACAAGACCCAGAGCT - 620
Db      |||||
Qy 643 TTTGATCAGAATGCGTTTCCATAGAATCTTTGAGCAACCGGAGACGCTGCTTACGATATC 702
Db      |||||

```

621 -----TGAGGCGCTGTAGAGAAAATTTTGAAGACACCGCGAGCTGCTCATCAT 675
 703 ATCAAGCGCAAGGCTTACTTATATGGAATCGCAGCGGGATTTACTTCCATAGTAAG 762
 676 ATGACGCCAAGGCTCCACTTCTACGGCATCGCATGGTCTTGTCTGCATCACCCGC 735
 763 GCGATTTTAGAGGATACAGGATCCACACTTACAGT---TTCAACCGTGTGTGATATTTT 819
 736 GCAATCTTCGAGAACCAAGGTTGGAGTCCAGTCTCTGCACTGCTCCAGGTGATAC 795
 820 GGGTTGAACAAATTTGCTATAAGCGTCCCTACCAAACTCAATAAAAGTGGGGCTCATCAA 879
 796 GGTGAGGAAGACATCTACATCGGCACCCAGCTGTGTGAACCGCCGAGGCATCCGCGC 855
 880 GTGCTGAACCTTCACTCGATGAGAAGAAATAGAAATGATGGAATAATCAGTAGT 936
 856 GTTGTGAACATAGAAATCAACCGACGAGATGGAACGCTTCAAGCATTCGCAAT 912

RESULT 7

US-09-738-626-1/c
 ; Sequence 1, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3309400
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1

Query Match 15.9%; Score 154.2; DB 11; Length 3309400;
 Best Local Similarity 50.8%; Pred. No. 3.2e-34;
 Matches 456; Conservative 0; Mismatches 423; Indels 18; Gaps 3;
 52 AACTGTTGGTAGTGGGAGTGGGAGTGGGCTGCCACAGGTATACGTTGCTTC 111
 3113369 AAGATTGTCTCATTTGGCGCAGGAGATGTTGGAGTTGCATACGATACGCACTGATCAAC 3113310
 112 AGCGGCATCGTTTCCGAGATTGCTTATCGACGTGAACAAAGACAGAGGGTGAA 171
 3113309 CAGGCGATGGCAGATCACCTTGGCATCATCGATCGATGAAGAACTCGAAGGCAAC 3113250
 172 AGCATGAGCTTAAACCAAGCA-----GCACCTTCAATAACAAGTCTTCGAGCGGGT 222
 3113249 GTCATGAGCTTAAACCAAGCTGTTGTGTGGGCCGATTCGCCACCCCGCTCACCAAGGGC 3113190
 223 GATTATCTGACTGCTGGCGCGCGCATTTGTTATTCATGTCATGCGGATTAACCAAAA 282
 3113189 ACCTACGCTGACTGCGAAGACGAGCCATGTTGTCATTTGTGCGCGGAGCCCAAG 3113130
 283 AATGACAAACAGGATGGATCTTGTGTCGAAAAAATGCCAACATTTATGCTGGAATCATC 342

3113129 CCAGGCGAGACCGCTCCAGCTGTGTGACAAAAAGTCAAGATTATGAAATCCATCGTC 3113070
 343 CCCAATGTTGCCAAATATGCTCTGATACCATCTCTGTTATTTGCGCACGAATCTCTGTCGAT 402
 3113069 GCGATGTCTATGACACAGCGGATTCGACGGCATCTTCTCTGCGCGTCCAAACCCAGTGGAT 3113010
 403 GTTTTGACCTATATAGCTATAGGGGTTCAGGGTTCCTCACTAAGCAGAGTTATCGGCTCA 462
 3113009 ATCTGACCTACGAGTGTGGAATTTCTCCGGCTTGGAAATGGAACCCGCGTATCGGCTCC 3112950
 463 GSTACAGTTCTCGATATCTGCTGTTTAAATACATCTCTCGGAGACACTTCAAGATCTCA 522
 3112949 GGAACGTCTCTGAGCTCCGCTCGATTCGCTACATGCTCGCGCAACTCTACGAAGTGGA 3112890
 523 TGGACAGCATGATGCTGCTGTGTAATTGGAGAACATGTTGATTCGGGTGTGCTGCTG 582
 3112889 CCAAGCTCCGCTCCACGCTTACATCATCGGCGAACACGGCGACACTGAACTTCCAGTCTG 3112830
 583 TCTCTTACCAACATCGACGCGCATGAGCTCCGGATTACTGCGAAAAAGCCACACATA 642
 3112829 TCTCCGCGACCATCGACGCGTATCGCTTAGCCGAATGCTGGACAAAGACCCAGAGCT- 3112771
 643 TTTGATCAGAATCGGTTCCATAGAAATCTTTGAGCAAAACGCGAGACGCTGTACGATATC 702
 3112770 -----TGAGGCGCTCTAGAGAAAATTTTGAAGACACCCGCGACGCTGCTATCAATT 3112716
 703 ATCAAGCGCAAGGCTATATCTTCATATGGAATGCGAGCGGATTAATCTTCGATAGTAAG 762
 3112715 ATCGACGCCAAGGGCTCCACTTCTACGCGATCGGATGGGTCTGCTCGCATCACCCGC 3112656
 763 GCGATTTTAGAGGATACAGGATCCACACTTACAGT---TTCAACCGTGTGTGATATTTT 819
 3112655 GCAATCTCGAAGAACCAAGAGTTGCGATGCCAGTCTGCACTGCTCCAGGTGATAC 3112596
 820 GGGTTGAACAAATGCTATAGCGTCCCTATCCAACTCAATAAAAGTGGGGCTCATCAA 879
 3112595 GGTGAGGAAGACATCTACATCGCACCCCGAGCTGTGTGAACCGCGAGGCAATCCCGCGC 3112536
 880 GTGCTGGAATTTCACTCGATGAGAAGAAATAGATTGATGGAATAATCAGTAGT 936
 3112535 GTTGTGAACTAGAAATCAACCGACGAGATGGAACGCTTCAAGCATTTCCGCAAT 3112479

RESULT 8

US-09-974-300-73
 ; Sequence 73, Application US/09974300
 ; Patent No. US20020146721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Clausen, Ib Groth
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; TITLE OF INVENTION: Expression
 ; FILE REFERENCE: 10085.500-US
 ; CURRENT APPLICATION NUMBER: US/09/974,300
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 09/680,598
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/279,526
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 8481
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 73
 ; LENGTH: 747
 ; TYPE: DNA
 ; ORGANISM: Bacillus licheniformis
 US-09-974-300-73

Query Match 15.5%; Score 151; DB 11; Length 747;
 Best Local Similarity 52.7%; Pred. No. 3.4e-35;
 Matches 375; Conservative 0; Mismatches 330; Indels 6; Gaps 2;
 226 TATCTGACTGCGCTGCGCGGCCATTGTTATTGTACATGTGGGATTAAACCAAAAAAT 285


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Db      2  TATGATGACTGCAAGAGCTGATATTTGTCGGGTATGCGCGAGCGAACCRAAAGCCG 61
Qy      286  GGACAAACAAGAGTGGATCTTGCTGCAAAAATGCCAAATATGCTGGAAATCATCCCC 345
Db      62  GGTGAACCCGCTTGATCTAGTCAAAAGAACTTGAATTTTAAAGGAATCATCGGA 121
Qy      346  AATGTTGCCAAATATGCTCTGATACCATCTGCTGTTATGCCAGAAATCTGTCGATGTT 405
Db      122  GAAGTCATGCGCCAGCGGTTTACCGCATCTTCTCGTCGCTACAAACCCCTGTCGATC 181
Qy      406  TTGACCTATATAGCTATAAGCGTCAAGGTTTCCACTAAGCAGAGTATTCGGCTAGGT 465
Db      182  TTGACTTATCGGACTTGGAATTCAGCGGCTTCCAAAGAAACGCGTCATCGAAGCGGC 241
Qy      466  ACAGTTCTGGATATGCTGCTTTTAAATACATCTCGGAGAGCACTTCAAGATCTCATCG 525
Db      242  ACAACGTTGACACTGCGGTTCCGCTACTTGTCTAGCAGATATTCGGTGTGCTGCC 301
Qy      526  GACAGCATGATGCTGTGTAATGGAGAAATGCTGTAATCGGCTGCTGCTGCTGCT 585
Db      302  CACAATCGCAGCGCTATATCAATGTTGTAACAGGATACGGAGCTGCTGCTGAGC 361
Qy      586  CTTACCAACATCGACGCTGAGCTCGGATTAAGCTGCAAAAGCAACCAACATATTT 645
Db      362  CATCGAATATCGCGGAGTTCCGCTCAGCG---ACTTGTCTGAAAGAAATGAGAAATAC 418
Qy      646  GATCAGAAATGCTTCCATAGAACTTTGAGCAACGCGAGCACTGCTTACGATATCATC 705
Db      419  AAAGCGAAGATCTAGATGAATCTTTGACAAATGTAAGAAACGCGCTTACCAATATT 478
Qy      706  AAGCGCAAGGCTATCTTATGAAATCGCAAGGATTAAGCTGCAATGTAAGAGCG 765
Db      479  GAGAAAGGCGGACATATCTAGGAGTTGCGATGAGCTCGCAGCTTACGAAAGCG 538
Qy      766  ATTTAGAGGATACAGATCCACACTTACAGTTTCAAC---CGTTGATGATATTTGG 822
Db      539  ATTTATCGAAATGAAGAAATTTTGAACGCTGAGCGCTCATCTGTGATGTAATTGGA 598
Qy      823  GTTGAACAAATGCTATAAGCGTCCCTTACCAACTCAATAAAGTGGGCTCATCAAGTG 882
Db      599  GAAATGATGTTTATATCGAGTTCCGCGGTTGTCGGCGATGCGGAGCGAGGAATT 658
Qy      883  GCTGAATCTTCTGATGAGAGGAATAGAAATGATGAAATCAAGCT 933
Db      659  GTTGAGCTCGATCTGAACGAAAGGAAACAAATTCAGCATCGCGCAGGT 709

RESULT 9
US-10-274-266-1
; Sequence 1, Application US/10274266
; Publication No. US20030059893A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins, Nucleic Acid Molecules Encoding
; FILE OF INVENTION: Secreted Proteins, And Uses Thereof
; FILE REFERENCE: CL000839DIV
; CURRENT APPLICATION NUMBER: US/10/274,266
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-274-266-1

Query Match      14.0%; Score 136; DB 15; Length 1146;
Best Local Similarity 49.7%; Pred. No. 1.5e-30;
Matches 380; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

Qy      52  AAAGTTGCTGATGGAGTGGGAAGTTGGTCTGCCACAGGCTATAGCTTCTCTC 111

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Db      211  AAGGCTCTCCATCATAGAAACTGGATCGTGGCGATGCGCTGCTATCAGCATCTTATTA 270
Qy      112  AGCGGATCGTTTCCGAGATTTGCTTATTCGAGCTGAACAAAGACAAAGCAGAGGGTGAA 171
Db      271  AAGGCTTGGATGATGATCTTGGCTTGGATCTTGTGATGAGACAAACTGAGAGGGTGAG 330
Qy      172  AGCATGGACTTAAACCCAGCAGCACCTTCAAATACAAAGTCT-----TCGAGCGGGT 222
Db      331  ACGATGGATCTTCAACATGCGAGCCCTTTCACGAAATGCAAAATATTTGTTGTAGCAA 390
Qy      223  GATTATCTGACCTGCGCTGCGCGGCGCATTTGTTGTCACATGTTGGATTAACCAAAA 282
Db      391  GATTATCTTGTTCACAGAAACTCCAACCTAGTGAATATATCACAGCAGGTGCACCCAGNA 450
Qy      283  AATGGCAAAACAAAGATGGATCTGCTGCAAAAATGCCAAATATGCTGGAAATCATC 342
Db      451  AAGGAGAAACGCGCTTAAATTTAGTCCAGCGAAATGTGGCCATCTTCAAGTTAATGATT 510
Qy      343  CCAATGTTTGCCTGCTGCTGATACCATCTGCTTATTCGCCAGAAATCTCTGTCGAT 402
Db      511  TCCAGTATTTCCAGTACAGCCCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 570
Qy      403  GTTTGACCTATATAGCTATAGCGCTGAGGCTGAGGCTTCCACTAAGCAGAGTATTCGCTCA 462
Db      571  ATCTTAACCTATAGTGTGGAAGTTGAGTGCATTTTCCAAAACCCGATTTATTTGGAAGC 630
Qy      463  GGTACAGTTCTGATATGCTGCTGCTTAAATATACATCTCGGAGAGCACTTCAAGATCTCA 522
Db      631  GGTGTAATCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
Qy      523  TCGACAGCATCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
Db      691  TCTGAAGCTGCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 750
Qy      583  TCTCTTACCAACATCGACGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
Db      751  AGTGGAGTGAACATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 810
Qy      643  TTTGATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
Db      811  AAGATCTGAGCAATGGAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 870
Qy      703  ATCAAGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
Db      871  ATTAAGTGAAGGTTTATCTTCTGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Qy      763  GCGATTTTAGAGTACAGATCCACATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 806
Db      931  AGTATTTTGAAGAACTTTAGGAGATATCATCCAGTTTCCACCAT 974

RESULT 10
US-09-731-872-14
; Sequence 14, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Homo sapiens

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Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SRIPI300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1938

LENGTH: 1062

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-1938

Query Match 12.7%; Score 123.6; DB 11; Length 1062;

Best Local Similarity 49.9%; Pred. No. 8.4e-27;

Matches 346; Conservative 0; Mismatches 339; Indels 9; Gaps 1;

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QY 52 AAGTTGTTGTTAGTGGAGTGGGAGTGGTGGTCTGCGACAGGTATAGTGTCTCTC 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 AAGTCTCGGTGCGAGTGGGAAAGTGGGATGGCCATAGCTCAACCATCTCACT 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 112 AGCGGCATCTTTCCGAGATGTCCTTATCGAGTGAACAAAGACAGAGGGTGAA 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 CAAGATCTCGACAGAGATGCTCTGTTGACGCCAACCCGATAGCTTCGTGGCAA 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 172 AGATGAGCTTAAACACAGCAGACCTTC-----AAATCAAGGTCGAGCGGGT 222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 ATGCTTGATCTCCAAACGCGCGTCTTCTCCTCGAACTAAGATCACCGTCTCTGT 303
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 223 GATTATCTGACGCGCTGGCGGCGCATGTTATTGTACATGTGGGATTACCAAAA 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 GATTACGAAGTACCGCTGGATCTGATCTTTGTATGTCATCTGCTGGTGTAGACAG 363
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 283 AATGGCAAAACAAGATGGATCTTGCTGCAAAAAATGCCAAATATGCTGGAAATCATC 342
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 364 CCAGCGAGCTAGACTCAATTTGCTTCAGAGGAACTGCTCTCTTCGTCATATCAT 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 343 CCATATGTTGCCAAATATGCTCTGATACCACTCTGCTTATGCGCAGAACTCTGCGAT 402
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 CCTCCACTCGCTAAAGCTTCTCCTGATTTATATGATCATTTGTTCTAATCCGTTGAT 483
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 403 GTTTTGACCTATATAGCTATAGGCGTCAAGGTTTCCACTAGCAGAGTTATCGGCTCA 462
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 GTTTTGACTTACGTTGCTGGAACTCTCTGGCTTTCCGGTGAATCGGGTCTTGGATCT 543
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 463 GGTACAGTCTTGGATATGCTGCTTTTAAATATACATCTCGGAGACACTTCAAGATCTCA 522
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 544 GGTACTAATCTCGATCTCTCGTCCGATTTCTTAATCGCAGATCATCTCGACGTTAAT 603
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 523 TCGCAGACATCGATGCTGTGTAATGGAGAACATGGTGAATTCGGGTGCTGCTG 582
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 604 GCTCAGGATGTACAGGCATTTATTTGGGAGAGCATGGACAGCTCAGTGGCATTTGTG 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 583 TCTCTTACCAACATCGACGCATGAGCTCCGGGATTTACTGCGAAAGACCAACATA 642
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 664 TCAAGCATTTAGTTGGAGGCATTTCTGCTTAAAGCTTTTGGAGAGAACCCAGATAGCT 723
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 643 TTTGATCAGAAATCGTTTCCATAGAACTTTTGGACAAACGGAGACGCTGCTTACGATATC 702
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 724 TACGAGAAACAAACTCTTTGAGGATATCCACCAAGCTGTTGTTGGTAGCGCTATGAGTG 783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 703 ATCAAGCGCAAGGCTATATCTTCATATGGAATCG 736
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Db 784 ATTGGACTCAAGGTTTACACTTCTTGGGCATTG 817

RESULT 13

US-09-971-361-1

Sequence 1, Application US/09971361

Patent No. US20020081677A1

GENERAL INFORMATION:

APPLICANT: Javed, Muhammad

APPLICANT: Cusdin, Fiona

APPLICANT: Milner, Paul

APPLICANT: Green, Edward

TITLE OF INVENTION: Ethanol Production

FILE REFERENCE: 000487,00010

CURRENT APPLICATION NUMBER: US/09/971,361

CURRENT FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: US 60/247,017

PRIOR FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: UK 0024554.8

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 4913

TYPE: DNA

ORGANISM: Bacillus strain TN

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(4913)

OTHER INFORMATION: n = A,T,C or G

US-09-971-361-1

Query Match 12.5%; Score 121.2; DB 10; Length 4913;

Best Local Similarity 54.1%; Pred. No. 1e-25;

Matches 293; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

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QY 377 TGCTTATTCGCACGAATCCTGTCGATGTTTTCACCTATATTAGCTATAAGCGTCAGGGT 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3758 TTCCTGTGCGACAGCAACCCAGTGGATATTTTAACTGCTACTTGGAAATTTAGCGGGT 3817
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 437 TTCCTAAGCAGAGTATTCGGCTCAGGTACAGTTCCTGGATATCTGCTGTTTAAATACA 496
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3818 TACCGAAAGAGCGGGTAAATCGGCTCAGGAACGATTTCTGATACAGCAAGATTCGGTCT 3877
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 497 TCTCGGACAGCATTCAGATCTCATCGGACAGCATCGATCGCTGTGTAATTTGGAGAAC 556
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3878 TGCTAAGTGAATATTTTCAAGTGGCTCCGACCAATGTACATGCTATATTTATTTGGCGAGC 3937
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 557 ATGGTGATTCGGGTGTGCTGCTGCTCTTACCAACATCGACGCAATGAAAGCTCCGGG 616
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3938 ATGGGATACAGAGTGGCTGCTGTTGGAGCATCGGAAATTTGAGCATTCAGTTGAGC 3997
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 617 ATTACTCGGAAAGCAACCAACATATTTGATCAGATCGGTTCCATAGAAATCTTTGAGC 676
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3998 AAATATGATGCAA---AACGATACTATAGAAAAGAGGATTTAGACAATACTTTGTTA 4054
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 677 AAACGGACAGCTGCTTACGATATCATCAAGGCAAGGCTATATCTTCATATGGAATCG 736
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4055 ATGTTGCTGATCGGCATATCAAAATCATTTGAGAAAAAGGGGCAACGATTTACGGCATTTG 4114
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 737 CAGCGGATTTACTTCGCATAGTAAAGGGCGATTTTAGAGGATACAGGATCCACATTTACAG 796
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4115 CAATGGATTTAGTCGTCATCTGCTGCTATTTTTCACATGAAATGCCATCTTAAACCG 4174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 797 TTTCAACCGTTCGTTGATT---ATTTGGGGTTGAACAAATTCCTATTAAGCGTCCCTACCA 853
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4175 TTTCTGCTCATTTGGACGGCCAAATATGGCGAACGAAATGTTTATATTTGGCGTCCCTGCCA 4234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 854 AACTCAATAAAGTGGGCTCATCAAGTGGCTGAATTTTCTGATGAGAGGAATAG 913
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4235 TTATCAACCGAAACGGTATTTCTGTAAGTGAATTTGACGCTAAATGAACAGAACAC 4294
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 914 AA 915
Db 4295 AA 4296

RESULT 14
US-09-731-872-15
; Sequence 15, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne, Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US3 REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 15
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..517
; NAME/KEY: sig_peptide
; LOCATION: 101..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.57613483592743
; OTHER INFORMATION: seq FLCLGMALCLRQA/TR
US-09-731-872-15

Query Match 12.4%; Score 120.8; DB 11; Length 1755;
Best Local Similarity 51.2%; Pred. No. 7.7e-26;
Matches 392; Conservative 0; Mismatches 357; Indels 17; Gaps 4;

QY 52 AAGTGTGGTGTGGAGTGGGAAGTGTGGGTCTGCGCACAGCGGTATAGCTGTCTTC 111
Db 311 AAGTGTCCATCATAGAACTGGATCGTGGCGATGCGCTATCAGCATCTTGTA 370

QY 112 AGCGCATCGTTCCGAGATTGCTTATCGACGTGAACAAAGCAAGAGGGGTGAA 171
Db 371 AAGGGCTTGAGTGATGAACCTTGGCCCTTGTGGATCTTGATGAAGACAAACTGAAGGGTGAG 430

QY 172 AGCATGGACTTAAACACGACGACCTTCAAAATCAAGGTCTCGAGCGGT-----G 223
Db 431 ACGATGGATCTTCAACATGCGAGCCCTTTCAGAAATGCCAATATTGTTGTAGCAAG 490

QY 224 ATTATCTGACTGGCGTGGCGGCCCATTTGTTATTGTCAATGTGGGATTAACCAAAAA 283
Db 491 ATTACTTTGTACAGCAAACTCCAACCTAGTGATTATCACAGAGGTGCGACGCAAGAA 550

QY 284 ATGACAAAACAGATGATCTTGTGCAAAAAATGCCAATATATGCTGGAATCATCC 343
Db 551 AGGAGAAAACCGCCCTTAATTTAGTCCAGCGAAATGTGGCCATCTT-CAAGTAATGATT 609

QY 344 CCAATGTTGCCAAATATGCTCTCATACCATCTGCTTTATTGCCACGAATCCTGTGATG 403
Db 610 CCAGTATGTCCAGTACAGCCCACTGCAACTGATTATTGTTCCAACTCAGTGATA 669

QY 404 TTTTGACCTATATTAGCTATAGGCGTTCAGGGTTTCCACTAAGCAGAGATTATCGGCTCAG 463
Db 670 TCTTAACTTATGTAGCTTGAAGTTGAGTGATTTCCAAAAACCGTATTATTGGAAGCG 729

QY 464 GTACAGTTCTGGATCTGCTGTTTTTAAATACATCTCGGAGAGCACTTCAAGATCTCAT 523
Db 730 GCTGTAATCTGGATCTGCTGTTTTTCTGTTTCTTTGATTTGGACAAAGCTTGGTATCCATT 789

QY 524 CGCACAGCATCGATGCTGTGTAATTTGGAGAACATGTTGCGGTGTGCTGTCTGTT 583
Db 790 CTGAAAGCTGCCCATGGATGATCTCTCGAGAGCATGGAGACTCAAGTGTCTTCTGTGGA 849

QY 584 CTCTTACCAACATCGACGGCATGAAGCTCGGGAT---TACTCGCAAAAGCAACACCA 640
Db 850 GTGGAGTGAACATAGCTGTGTCCTTTGAAGGATCTGAACCTCTGATATAGGAACATGATA 909

QY 641 TATTTGATCAGATGCGTTCCATAGAAATCTTTGAGCAAAAGCGAGAGCGTCTTAGATA 700
Db 910 AAGATCTCTGAGCAGG-----AAAAATGTCCACAAAGAAGTGAAGTCAACTGCGCTATGAGA 964

QY 701 TCATCAAGCGCAAGGCTATCTATCTATGAAATCGCAGCGGATTTACTTCGCATAGTAA 760
Db 965 TTATTAATGAAGGTTTATCTTCTTGGCCATTTGGCCATCTGTCGCGGATTTAACAG 1024

QY 761 AGCGGATTTTAGAGGATACAGGATCCACACTTTACAGTTTCAACCGT 806
Db 1025 AAAGTATTTTGAAGATCTTAGGAGAAATACATCCAGTTTCCACCAT 1070

RESULT 15
US-09-974-298-74
; Sequence 74, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 74
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 3365683CB1
US-09-974-298-74

Query Match 11.3%; Score 109.8; DB 11; Length 1172;
Best Local Similarity 47.7%; Pred. No. 1.3e-22;
Matches 361; Conservative 0; Mismatches 387; Indels 9; Gaps 1;

QY 61 GTAGTGGGAGTGGGAAGTGTGGGTCTGCCACAGCGGTATACGTTGCTTCTCAGCGGCATC 120
Db 191 GTAGTGGGTGTGGACAAGTGTGTATGGCGTGTGCTATCAGCATTTGGGAAAGTCTCTG 250

QY 121 GTTTCGAGATTGCTTATTCGACGTGAACAAAGACAAAGAGAGGGTGAAGCATGGAC 180
Db 251 GCTGATGAATGCTCTTGTGGATGTTTGGGAAGATAAGCTTAAAGAGAGAAATGATGGAT 310

QY 181 TTAACACAG-----CAGCACCTTCAATACAGGCTCTCGAGCGGGTGAATTCCT 231
Db 311 CTGCAGCATGGGAGCTTATTTCTTCAGACACCTTAAATTTGTGCAGATAAAGATTTCT 370

QY 232 GACTGCGCTGGCGCGGCCCATTTGTTATGTCAATGTGGGATTAACCAAAAAAATGACAA 291
Db 371 GTGACCGCCAAATCTAAGATTGTAGTGTAACTGCGAGAGTCCGTGAGCAAGAGGGAG 430

QY 292 ACAAGGATGGATCTTCTGCTCAAAAAATGCCAATATATGCTGGAATCATTCCTCAATGTT 351
Db 431 AGTCGCTCAATCTGCTGCGAGAGAAATGTAATGTCTTCAAAATTCATTATTCCTCAGATC 490

QY 352 GCCAAATATGCTCTGATACCATCTGCTTATTCACCAAGATCTCTGCTGATGTTTTCACC 411
Db 491 GTCAGTACAGTCTGATTCATTAATTTGTTGTTTCCAACTTCCAGCGAGTTCCTTACG 550

QY 412 TATATTAGCTATAAGGCGTCAGGGTTTCCACTAAGCAGAGATTATCGGCTCAGGTACAGTT 471

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 08:17:36 ; Search time 1718 Seconds
(without alignments)
9162.988 Million cell updates/sec

Title: US-09-992-430B-21

Perfect score: 972

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:**

1: em_estba:**

2: em_esthum:**

3: em_estin:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: gb_gss:**

18: em_gss_hum:**

19: em_gss_inv:**

20: em_gss_pln:**

21: em_gss_vrt:**

22: em_gss_fun:**

23: em_gss_mam:**

24: em_gss_mus:**

25: em_gss_other:**

26: em_gss_pro:**

27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	152	15.6	968	17	CNS06Y1R
2	135	13.9	936	14	BQ963532
3	134.8	13.9	1058	13	BI410782
c 4	133.4	13.7	2603	17	BH770979
5	131.6	13.5	913	14	BQ895234
6	131.6	13.5	918	14	BQ955812

7	131.6	13.5	1032	13	BI410482
8	131.4	13.5	891	13	BI905403
9	131.4	13.5	1097	9	AU090981
10	130.8	13.5	951	14	BQ895574
11	130.6	13.4	903	14	BQ884746
12	130	13.4	959	14	BQ886472
c 13	129.8	13.4	645	17	CNS06YKH
14	129.8	13.4	926	14	BQ899735
15	129.6	13.3	924	13	BG916902
16	128.8	13.3	894	13	BI904831
17	128.8	13.3	1076	14	BQ818069
18	127.4	13.1	902	14	BQ886973
19	126.6	13.0	1129	13	BM464639
20	126	13.0	824	13	BI905607
21	126	13.0	1082	13	BM476010
22	125.8	12.9	1108	13	BM462026
23	125.6	12.9	710	14	BQ571108
24	125.6	12.9	818	13	BG915740
25	125.4	12.9	854	13	BI410650
26	125.2	12.9	944	9	AL559924
27	125	12.9	920	9	AL532872
28	125	12.9	947	9	AL543215
29	125	12.9	964	9	AL545000
30	125	12.9	1020	9	AL554514
31	125	12.9	1021	9	AL553512
32	125	12.9	1023	9	AL514320
33	125	12.9	1023	9	AL550051
34	124.6	12.8	949	14	BQ650107
35	124.6	12.8	965	9	AL552670
36	124.6	12.8	1017	9	AL559984
37	124.2	12.8	963	9	AL559795
38	124	12.8	999	9	AL541618
39	124	12.8	1059	13	BM450615
40	123.8	12.7	958	9	AL513680
41	123.6	12.7	741	14	BQ870980
42	123.6	12.7	842	9	AL541794
43	123.4	12.7	967	9	AL549487
44	123.4	12.7	967	14	BQ956047
45	123.2	12.7	872	14	BQ212714

ALIGNMENTS

RESULT 1	CNS06Y1R/c	968 bp	DNA	linear	GSS 06-JUL-2001
LOCUS	T3 end of clone AY0AA005E09 of library AY0AA from strain CBS 6340				
DEFINITION	of Kluyveromyces thermotolerans, genomic survey sequence.				
ACCESSION	AL420469				
VERSION	AL420469.1	GI:12203655			
KEYWORDS	GSS.				
SOURCE	Kluyveromyces thermotolerans.				
ORGANISM	Kluyveromyces thermotolerans				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.				
AUTHORS	1 (bases 1 to 968) Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)				
MEDLINE	20584711				
PUBMED	11152876				
REFERENCE	2 (bases 1 to 968)				
AUTHORS	Malpertuy, A., Llorente, B., Blandin, G., Artiguenave, F., Wincker, P. and Dujon, B.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 10. Kluyveromyces thermotolerans				

JOURNAL FBBS Lett. 487 (1), 61-65 (2000)
 MEDLINE 20584720
 PUBMED 11152885
 REFERENCE 3 (bases 1 to 968)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen
 yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES
 source Location/Qualifiers
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 /organism="Kluyveromyces thermotolerans"
 /strain="CBS 6340"
 /db_xref="taxon:4916"
 /clone="AY0AA00509"
 /clone_lib="AY0AA"
 /note="end : T3"
 complement(4..357)
 /note="similar to *Saccharomyces cerevisiae* ORF YDL078c [
 MDH3 ; malate dehydrogenase, peroxisomal]"
 /evidence=not experimental

misc_feature
 279 a 199 c 218 g 267 t 5 others

BASE COUNT 279 a 199 c 218 g 267 t 5 others

ORIGIN

Query Match 15.6%; Score 152; DB 17; Length 968;
 Best Local Similarity 66.2%; Pred. No. 1.5e-33;
 Matches 237; Conservative 0; Mismatches 115; Indels 6; Gaps 1;

Qy 38 ATGCAAAACAGTAAAGTTGCTGAGTGGGAGTGGGAGTGGGCTGCGCACAGCGT 97
 Db 368 AAGTGAACCTTGCTCAAGTTGCTGTTATGTTGTTGGAGTGGGCTCTACTACGSCCT 309
 Qy 98 ATACGTTGCTTCTCAGCGGCATCGTTTCCGAGATGTCTTATCGACGTGAACAAAGACA 157
 Db 308 ACACCTGCTATTAGCGAGATGATCTCGGAAGTTGTTGATTGATCAACACACATA 249
 Qy 158 AAGCAGAGGGTGAAGCATGACCTTAAACACGAGCAGCCTTCAAAATACAAAGTCTCGAG 217
 Db 248 AAGCAGAGGGCGAAGCATGGAATTAACCATGCTGCACCTTCCACAAACAGGTTCTGTTG 189
 Qy 218 CG-----GGTGATTCTCAGCTGCGCTGCGCGGCGCATTTGTTATGTCACATGTGGGA 271
 Db 188 TGTATGTTGGAGATTATAGCGACTGCGCGGCGCTGCGGATTTGATCAATTACAGTGGCG 129
 Qy 272 TTAACCAAAAATATGGAACAAAGGATGGATCTTGTGTCGCAAAAATATGCCAATATTATGC 331
 Db 128 CCAATCAAAAACCTGGTCAACTAGATGGAATTTAGCAGCAACAAACGCAAGATCTTAC 69
 Qy 332 TGGAAATCATCCCAATGTTGCCAAATATGCTCTGTATGATCACCATCCTGCTTATGGCCAC 389
 Db 68 AAGGTATTATTCCCAAGATAGTTGAGTACGCGCCCAAAAATATTCTTCTCATTTGCCAC 11

RESULT 2
 BQ963532 936 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT 10050420 NIH MGC 134 Mus musculus cDNA clone
 DEFINITION IMAGE:6514321 5', mRNA sequence.
 ACCESSION BQ963532
 VERSION BQ963532.1 GI:22379010
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 936)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. David Rowe
 CDNA Library Preparation: Invitrogen Corp
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM14089 row: h column: 02
 High quality sequence stop: 683.
 Location/Qualifiers
 1..936
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:6514321"
 /clone_lib="NIH MGC 134"
 /tissue_type="undifferentiated limb"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2:
 NotI; Cloned unidirectionally. Primer: Oligo dt. Average
 insert size 1.7 kb. Constructed by ResGen, Invitrogen
 Corp. Note: this is a NIH MGC Library."
 BASE COUNT 223 a 237 c 264 g 212 t

ORIGIN

Query Match 13.9%; Score 135; DB 14; Length 936;
 Best Local Similarity 51.1%; Pred. No. 1.5e-28;
 Matches 349; Conservative 0; Mismatches 325; Indels 9; Gaps 1;

Qy 52 AAAGTTGTGCTAGTGGGAGTGGGAGTGGTGGTCTGCCACAGCGTATACGTTGCTTCTC 111
 Db 173 AAGATTACAGTTGTTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 232
 Qy 112 AGCGGATCGTTTCGAGATTTGCTTATCGAGGTGAACAAAGACAAAGCAGAGGTGAA 171
 Db 233 AAGGACTTGGCGGATGAGCTTGCCTTGTGACGTATGGAAGACAACTCAAGGGCGAG 292
 Qy 172 AGCATGGACTTAAACCAACGACGACCTTCAAAATACAAAGTCTCGAGCGGTGATTATCCT 231
 Db 293 ATGATGGATCTCCAGATGGGAGCTCTTCTTTAAACACCAAAATTTGTCTCAGCAA 352
 Qy 232 GACTGCGCTGGCGCGGCCA-----TTGTTATTGTCAATGTGGGATTAACCAAAA 282
 Db 353 GACTACTGTGTAACTCGGAATCCAGCTGGTCAATTATCACCGGGGGCGCGTCAGCAA 412
 Qy 283 ATGGCAACAAAGGATGGATCTTGTGCAAAAATGCCAATATGTCGGAATCAATC 342
 Db 413 GAGGGGAGAGCGGGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTCAAT 472
 Qy 343 CCCAATGTTGCCAAATATGCTCTGATACCATCTCTGTTATTGCCACGAATCTCTGCGAT 402
 Db 473 CCCAATGTTCAAGTACAGTCCACTGCAAGCTGCTGATCTGCTCAATCCAGTGGAT 532
 Qy 403 GTTTTGACCTATATTAGCTATAAGGCGTCAAGGTTTCCACTAAGCAGAGATTATCGGCTCA 462
 Db 533 ATCTTGACCTAGCTGGCTTGGAAATATCAGTGGCTTTCCCAAAAACCGAGTATTTGGAAGT 592
 Qy 463 GGTACAGTTCTGGATCTGCTGTTTTTAAATATCATCTCTGGAGAGCACTTCAAGATCTCA 522
 Db 593 GGTGCAATCTGGAATTCAGCGCGGTTCCGTTACCTGATGGGAGAGGCTGGGGGTTAC 652
 Qy 523 TCGGACAGCATCGATCGCTGTGTAAATGGAGAACATGGTGTATTCGGGTGTGCTGTCTGG 582
 Db 653 GCGCTGAGCTGTCAACGCTGGGTTCCTGGGAGAACATCGGCACTCCAGTGTGCTGTGTTG 712
 Qy 583 TCTCTTACCAACATCGACGGCATGAAGCTCCGGGATTATCTCGGAAAAGCCAAACCATTA 642


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Db      713 AGTGGTGTGAATGTGCGCGCTCCCTGAAGTCTCTTAACCCAGAACTGGGCACTGAC 772
QY      643 TTTGATCAGAAATGGTTCCATAGAACTTTTGGACAAACGGAGCGCTGCTTACGATATC 702
Db      773 GCAGACAGGAGCAGTGGGAGAGTTCAACAGCAAGTGTGGACAGTGCCTACGAGGTG 832
QY      703 ATCAAGCGCAAGGCTATATTC 725
Db      833 ATCAAGCTGAAGGTTACATC 855

RESULT 3
LOCUS   BI410782
DEFINITION 602963554F1 NCI_CGAP_Lu33 Mus musculus cdna clone IMAGE:5119236 5', mRNA sequence.
ACCESSION BI410782
VERSION 1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1. (bases 1 to 1058)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1290 row: k column: 13
High quality sequence start: 30
High quality sequence stop: 917.
FEATURES
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        1..1058
            /organism="Mus musculus"
            /strain="CZECH II"
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            /clone="IMAGE:5119236"
            /clone_lib="NCI_CGAP_Lu33"
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            /lab_host="DH10B (phage-resistant)"
            /notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; let strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5]. TGTACCAATCGAAGTGGAGCGCGCTCGTTTGTCTTTTGTCTT 3'}. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 265 a 258 c 293 g 242 t
ORIGIN

Query Match 13.9%; Score 134.8; DB 13; Length 1058;
Best Local Similarity 50.1%; Pred. No. 1.9e-28;
Matches 368; Conservative 0; Mismatches 357; Indels 9; Gaps 1;

QY      52 AAAGTTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGGATACGTGCTTCTC 111
Db      152 AAGATTACAGTTGTGGGTTGGTGTGGCATGCTGTGCCATCAGTATCTTAATG 211
QY      112 AGCGGCATCGTTTCCGAGATGTCCTTATCGATGCAAGTGAACAAAGACAGAGGGTGA 171

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Db      212 AAGGACTTGGCGATGAGCTTGCCCTTGTGTGACGTGATGAAAGACAAACTCAGGGCGAG 271
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QY      232 GACTGCGCTGGCGCGGCCA-----TTGTTATTTGTCAATGTGGGATTAAACCAAAA 282
Db      332 GACTACTGTGTAACTCGGAATCCAAAGCTGGTCATTATCACCGCGGGGCCGCTCAGCA 391
QY      283 AATGGACAAACAGGATGGATCTTGTCTCAAAAAATGCCAAATTTATGTGGAATATC 342
Db      392 GAGGGGGAGCGCGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTTCATCAT 451
QY      343 CCCAATGTTGCCAAATATGCTCTGATACCATCTCTTTATTCGCCACGAATCTGTGCGAT 402
Db      452 CCCAATTTGTCAAGTACAGTCCACACTGCAAGCTGCTGATCGTCTCCAATCCAGTGGAT 511
QY      403 GTTTTGACCTATATTAGCTATATAAGCGCTCAGGGTTTCCACTAAGCAGAGTTATCGGCTCA 462
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QY      463 GGTACAGTTCTGGATACCTGCTGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCA 522
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QY      523 TCGGACAGCATCGATGCTGTGTAATTGAGAACATGGTGATTTCGGGTGTGCTGTCTGG 582
Db      632 GGCTGAGCTGTCAAGCTGGGCTGGGAGAACATGGGCACTCCAGTGTGCTGTGTGG 691
QY      583 TCTTTTACCAACATCGACGGCATGAAGTCCGGGATTACTGCGAAAAAGCCAAACCATATA 642
Db      692 AGTGGTGTGAATGTTGCGCGGCTCTCCCTGAAGTCTCTTTAAACCCAGAACTGGGCAC 751
QY      643 TTTGATCAAGATCGCTTCCATAGATCTTTGAGCAACCGGAGACGCTGTTACGATATC 702
Db      752 GCAGCAAGGAGCAGTGGAGAGGTTTCAAGCAGGTGTGGACAGTGCCTACGAGGTG 811
QY      703 ATCAAGCGCAAGGCTATATCTTCATATGGAATCGACGCGGGATTACTTCGCATAGTAAAG 762
Db      812 ATCAAGCTGAAGGTTACACATCTCTGGGCCATGGCCCTCTCTGTGGCAAGACTTGGTGA 871
QY      763 GCGATTTTAGAGGA 776
Db      872 GCATATGAAGAA 885

RESULT 4
BH770979/c
LOCUS   BH770979
DEFINITION LLMGtag704 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, DNA sequence.
ACCESSION BH770979.1
VERSION 1
KEYWORDS GI:20373936
SOURCE GSS.
ORGANISM Lactococcus lactis subsp. cremoris.
REFERENCE Lactococcus lactis subsp. cremoris Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
AUTHORS 1 (bases 1 to 2603)
TITLE Bolotin,A., Ehrlich,S.D. and Sorokin,A.
JOURNAL Studies of genomes of dairy bacteria Lactococcus lactis Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
Best homologue in strain IL1403 is ldh (100%)
Class: shotgun
High quality sequence start: 30

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High quality sequence stop: 2575.
 Location/Qualifiers
 1. .2603
 /organism="Lactococcus lactis subsp. cremoris"
 /strain="MG1363"
 /db xref="taxon:1359"
 /clone_lib="MG1363 Random Sequence Tag Library"
 /note="Vector: pSGM2; Site 1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
 743 a 550 c 496 g 814 t
 BASE COUNT 743 a 550 c 496 g 814 t
 ORIGIN

Query Match 13.7%; Score 133.4; DB 17; Length 2603;
 Best Local Similarity 50.2%; Pred. No. 7.4e-28;
 Matches 388; Conservative 0; Mismatches 376; Indels 9; Gaps 2;

35 CTGATGCCAAACAGTAAAGTTCTGGTAGTGGGAGTGGGAAGTGTGGGTCTGCCACAG 94
 1895 CTGATAACACACGTAAAGAGTTATCTTGTGTGACGGTGTGTAGGTTCATACAG 1836
 95 CGTATAGCTTCTCTCAGCGGCATCGTTCCGAGATTTGCTTATCGAGTGAACAAAG 154
 1835 CTTTGTGCTTGTAAACCAAGGAATTGCACAAGAAATTAGGTATTTGTGACCTTTTAAAG 1776
 155 ACAAAGCAGAGGGTGAAGCATGACCTTAACCA-----CGCAGCACCCTCAATACAA 208
 1775 AAAAAATCAAGGGGATGCAGAAGACCTTTCTCATGCTTGGCGATTTTACATACCTTAA 1716
 209 GGTCTCAGCGGGTGAATATCTCAGCTCGCTGCGCGGGCATTTGTTATTTGTCCATGTG 268
 1715 AGATTACTCTGCAGACTACTCTGATGCAAGGAGCTGACCTGTTGTCTGACTCTG 1656
 269 GGATTAACCAAAAAATGGCAAAACAAGGATGGATTTGCTGCAAAAAATGCCAACATTA 328
 1655 GTGCTCCACAAAAACCAAGGTGAATCTGCTTGACCTTTGTTGAAAAAATCTTCGTATTA 1596
 329 TGCTGGAATCATCCCAATGTTGCCAATATGCTCTGATACCATCTCTGTTATGCCA 388
 1595 CTAAGATGTTGTAACATAAATTTGTTGTTTCAAGGAAATCTTCTGCTGCTG 1536
 389 CGAATCTCTGCTGATGTTTGAACCTATATTTAGCTATAAGGGTTCAGGGTTTCCATAGCA 448
 1535 CTAACCCAGTTGACATCTTGACATACGCAACTTGGAAATCTCTGTTTCCCTAARAAC 1476
 449 GAGTTATCGGCTCAGGTACAGTTCCTGGATCTGCTGTTTAAATACATCTCTGGAGAGC 508
 1475 GTGTTGTAGTTTCAAGTACTTCACTTGATATGACACGTTTCCGCTCAAGCATTTGCTGAAA 1416
 509 ACTTCAAGATCTCATCGACAGCATCGATGCTGTGTAATTTGGAGAACATGTTGATTCGG 568
 1415 AAGTTAGTTGATGCTGCTTCAACATCAACGATACATCATGTTGGTGAACACGGTACTCAG 1356
 569 GTGTGCTGCTGCTGCTCTTACCAACATCGACGGCATCAAGCTCCGGGATTTACTGCGAAA 628
 1355 AATTGCTGTTGTTGTCACAGCTAAGCTGCTGTTGTTAAATTT---GGAACAATGGTTCC 1299
 629 AAGCAACCAATATTTGATCAGAAATCGGTTTCCATAGAACTTTTGAGCAACCGGAGACG 688
 1298 AAGAAATGACTACCTTAAACGAAGCAAAATCGTTGAAATTTGTTGAGTCTGTACGTGATG 1239
 689 CTGCTTACGATATCATCAAGCGCAAGGCTATATCTTCATATGGAATCGCAGCGGATTAC 748
 1238 CAGCTTACTCAATCATCGCTTAAAGAGGTGCAACATTTACGGTGTGGCTGTAGCCCTTG 1179
 749 TTCATAGTAAAGCGGATTTTAGAGGATACAGGATCCACACTTACAGTTTCA 801
 1178 CTCGTATTACTAAGCAATTTCTTGATGATGAACATGACGACTTCTCTGTATCA 1126

RESULT 5
 BQ895234
 LOCUS

AGENCY: 8752520 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6333286
 5', mRNA Sequence.
 BQ895234
 VERSION BQ895234.1 GI:22287248
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 913)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgebs-r@mail.nih.gov
 Tissue Procurement: Mark Macconochie, Ph.D. and Nancy L. Freeman, Ph.D.
 cDNA Library Preparation: ResGen, Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM13792 row: d column: 23
 High quality sequence stop: 740.
 Location/Qualifiers
 1. .913
 /organism="Mus musculus"
 /db xref="taxon:10090"
 /clone="IMAGE:6333286"
 /clone_lib="NIH MGC 130"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: oocytes; Vector: pCMV-SPORT6.1.cdb;
 Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
 Primer: Oligo dt. Average insert size 1.95 kb.
 Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."
 BASE COUNT 219 a 232 c 255 g 206 t 1 others
 ORIGIN

Query Match 13.5%; Score 131.6; DB 14; Length 913;
 Best Local Similarity 50.6%; Pred. No. 1.5e-27;
 Matches 351; Conservative 0; Mismatches 334; Indels 9; Gaps 1;

52 AAAGTTGCTGGTAGTGGAGTGGAGTGGTGGTCTGCCACAGCTATAGTGTCTTC 111
 153 AAGATTACAGTTGTTGGGGTGTGCTGTGGCATGGCTTGTGCCATCAGTATCTTAATG 212
 112 AGCGGCATCGTTTCCGAGATTGTCTTATCGAGTGAACAAACAAAGCAGAGGTGAA 171
 213 AAGGACTTGGCGATGAGCTTGGCCCTTGTGAGTCTATGGAGACAACTCAAGGGCGAG 272
 172 AGCATGCACTTAAACCAACGACACCTTCAAAATACAAAGTCTCGACGGGTGATTATCCT 231
 273 ATGATGGATCTCCAGCATGGCAGCTCTTCTTAAACACCAAAAATTTGCTCCAGCAA 332
 232 GACTGGCTGGCGCGGCCA-----TTGTTATTTGTCATGTGGGATTAAACCAAAA 282
 333 GACTACTGTGTAACCTCGAACTCAAGCTGGTCTTATCACCAGGGGGGCCCTCAGCAA 392
 283 AATGGCAAAACAAAGGATGATCTTGTGCAAAAAATGCCAATATTGTTGGAATCATC 342
 393 GAGGGGAGAGCGGCTCACTGTTGCCAGGAAAGTGAACATCTTCAAGTTTCATTT 452
 343 CCAATGTTGCCAAATATGCTCTGATACCATCTCTTATTTGCCAGAAATCTCTGCGAT 402
 453 CCACCAATTTCAAGTACAGTCCACACTGCAAGCTGCTGATCTCTCAATCCAGTGGAT 512
 403 GTTTTCACTTATTTAGCTATAGGCGTCCAGGGTTTCCACTAGCAGAGTTATCGGCTCA 462
 513 ATCTTGACCTACGCTGGCTTGGAAAAATCAGTGGCTTTTCCAAAAACCGAGTAATTTGAGT 572
 463 GGTACAGTTCTGATACTGCTCGTTTTTAAATACATCTCTCGAGAGCAGCTTCAAGATCTCA 522

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Db      573 GGTGCAATCGATTGAGCGCGGTTCCGTTACCTGATGGAGAGAGGCTGGGGGTTTCAC 632
Qy      523 TCGGACAGCATCGATGCTGTGTAATGGAGAACATGGTGAATTCGGGTGTCCTGTCTGG 582
Db      633 GCCTGAGCTGTACGCGTGGGTCCTGGGAGAACATGGCAGCTCCAGTGTGCTGTGTGG 692
Qy      583 TCTCTTACCAACATCGACGCGCATGAAGCTCCGGGATTACTGCGAAAGAACCAACACATA 642
Db      693 AGTGGTGTGAATGTGCGCGGCTCCCTCAAGTCTCTTAACCCAGAACTGGGCACTGAC 752
Qy      643 TTTGATCAGATGGTTCATAGAACTTTGAGCAACGCGAGACGCTGCTTACGATATC 702
Db      753 GCAGACAAGAGCAGTGGAGAGGTTTCAACAGCAGGTGGTGACAGTGCCTACGAGGTG 812
Qy      703 ATCAAGCGCAAGGCTATATCTTCATATGGAATCG 736
Db      813 ATCAAGCTGAAGGTTACATCTCTGGGCCATTG 846

RESULT 6
BO955812
LOCUS      BO955812
DEFINITION AGENCOURT_8752602 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6335643
5', mRNA sequence.
ACCESSION BO955812
VERSION    BO955812.1 GI:22371290
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    1 (bases 1 to 918)
TITLE      NIH-MGC http://mgi.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13798 Row: g Column: 04
High quality sequence stop: 716.
FEATURES
source
1. .918
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/db xref="taxon:10090"
/clone="IMAGE:6335643"
/clone_lib="NIH_MGC_130"
/lab host="DHI0B (phage-resistant)"
/notes="Organ: oocytes; Vector: pCMV-SPORT6.1.cdb;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
NIH MGC Library."
BASE COUNT 222 a 223 c 261 g 212 t
ORIGIN
Query Match 13.5%; Score 131.6; DB 14; Length 918;
Best Local Similarity 50.6%; Pred. No. 1.5e-27; Gaps 1;
Matches 351; Conservative 0; Mismatches 334; Indels 9;

Qy      52 AAAGTTGTGTAGTGGAGTGGGAAGTGTGGGTCTGCCACAGCGATACGTTGCTTCTC 111
Db      101 AAGATTACAGTTGTGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 160
Qy      112 AGCGGCATCGTTTCCGAGATTGCTTATCGATCGTGAAACAAAGCAGAGGAGTAA 171

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Db      161 AAGGACTTGGCGGATGAGCTTGCCCTTGTGTGAGCTCATGGAGACAAAACCTCAAGGGCGAG 220
Qy      172 AGCATGGACTTAAACCAACAGCAGCACCTTCAAATACAAAGTCTCGAGCGGGTGATTTATCCT 231
Db      221 ATGATGGATCTCCAGATGGCAGCCTCTTCTTTAAACACCAAAAATTTGTCTCAGCAA 280
Qy      232 GACTGCGCTGGCGCGGCCA-----TTGTTATTGTTCACATGTGGGATTAACCAAAAA 282
Db      281 GACTACTGTGTAATCTCGAACTCCAAGCTGGTTCATTATCACCGCGGGGCCGCTCAGCAA 340
Qy      283 AATGGACAACAGAGATGGATCTTGTCTCAAAAAATGCCAATTAATGCTGGAATATC 342
Db      341 GAGGGGGAGAGCGCGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTTCATCAT 400
Qy      343 CCCAATGTTGCCAAATATGCTCTCTGATACCATCTCTCTTATTGCCACAGAACTCTGTCGAT 402
Db      401 CCCAATTTGTCAAGTACAGTCCACACTGCAAGCTGCTGATCTCTCCATCCAGTGGAT 460
Qy      403 GTTTTGACCTATATTAGCTATAAGCGCTCAGGGTTTCCACTAAGCAGAGTTATCGGCTCA 462
Db      461 ATCTTGACCTACGTGGCTTGGAAATCACTGGCTTTCCCAAAAACCGAGTAATTGGAAGT 520
Qy      463 GGTACAGTTCTGGATACCTCTGTTTAAATACATCTCTCGAGAGCAGCTTCAAGATCTCA 522
Db      521 GGTGCAATCTGGATTCAGCGCGGTTCCGTTACCTGATGGAGAGGCTGGGGGTTTCAC 580
Qy      523 TCGGACAGCATCGATGCTGTGTAATTGAGAACATGTTGATTCGGGTGTGCTGCTGCTGG 582
Db      581 GGCTGAGCTGTACGCGTGGGTCCTGGGAGAACATGGCGACTCCAGTGTGCTGTGTGG 640
Qy      583 TCTTTTACCAACATCGACGCGCATGAAGTCCCGGATTACTGCGAAAAAGCCACACATA 642
Db      641 AGTGGTGTGAATGTTGCGCGGCTCTCCCTGAAAGTCTCTTAAACCCAGAACTGGGCACTGAC 700
Qy      643 TTTGATCAAAATGCGTTCCATAGATCTTTGAGCAAAACGGAGACAGCTGCTTACGATATC 702
Db      701 GCAGACAAGGAGCAGTGGGAAGGAGGTTTCAACAGCAGGTGTTGACAGAGTGCCTACGAGGTG 760
Qy      703 ATCAAGCGCAAGGCTATATCTTCATATGGAATCG 736
Db      761 ATCAAGCTGAAGGTTACACATCTCTGGGCCATTG 794

RESULT 7
BO955812
LOCUS      BO955812
DEFINITION AGENCOURT_8752602 NIH_MGC_130 Mus musculus cDNA clone IMAGE:5118756 5',
mRNA sequence.
ACCESSION BO955812
VERSION    BO955812.1 GI:15171405
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    1 (bases 1 to 1032)
TITLE      NIH-MGC http://mgi.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11289 Row: g Column: 13
High quality sequence start: 33
High quality sequence stop: 949.
FEATURES
Location/Qualifiers

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/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5118756"
/clone_lib="NCI CGAP Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5].
TGTTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 251 a 255 c 290 g 236 t
ORIGIN
Query Match 13.5%; Score 131.6; DB 13; Length 1032;
Best Local Similarity 50.6%; Pred. No. 1.6e-27;
Matches 351; Conservative 0; Mismatches 334; Indels 9; Gaps 1;
Qy 52 AAAGTTGTTGGTGGAGTGGGAAGTGGTGGTCTGCCACAGGTATACGTGCTTCTC 111
Db 165 AAGATTACAGTTGTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 224
Qy 112 AGCGGATCGTTTCCGAGATTGCTTATCGACGTGAACAAAGACAAAGAGGGTGAA 171
Db 225 AAGGACTTGGCGGATGAGTTGGCTTGTGACGTGATGAAGACAACTCAAGGGCGAG 284
Qy 172 AGCATGACTTAACACGACGACCTTCAATACAAAGTCTCGAGCGGTGATATCCT 231
Db 285 ATGATGATCTCCAGCATGCGAGCTCTTCTTAAACACCAAAATTTGCTCAGCAAA 344
Qy 232 GACTGCGTGGCGGGCA-----TTGTTATTGTCACATGTGGGATTAAACAAAAA 282
Db 345 GACTACTGTGTAATCTGGAACCTCAAGCTGTCATTAACACGGGGGGCGGTACGAA 404
Qy 283 AATGACAAACAAAGATGGATCTTGTGTCAAAAATGCCAACATATGCTGGAATCATC 342
Db 405 GAGGGGAGAGCGGCTCAACCTGTCAGCGAAACGTGAACATCTTCAAGTTTCATCAT 464
Qy 343 CCGAATGTTGCAATATGCTCTGATACCATCTCTGTTATGTCACGAATCTCTGAT 402
Db 465 CCGAATGTTGCAATATGCTCTGATACCATCTCTGTTATGTCACGAATCTCTGAT 524
Qy 403 GTTTTGACCTATATTAGCTATAAGCGGTTCAGGGTTTCCACTAAGCAGATTATCGGCTCA 462
Db 525 ATCTTGACCTACGTGGTGGAAATCAGTGGCTTTCACAAACCCAGTAATTTGGAAT 584
Qy 463 GGTACAGTTCTGGATCTGCTGTTTAAATACATCTCGAGAGACATTTCAAGATCTCA 522
Db 585 GGTGCAATCTGGATTGAGCGGCTTCGTTTACCTGATGGAGAGAGCTGGGGGTTTCA 644
Qy 523 TCGACAGCATCGATGCTGTTGTAATTGGAGAACATGTTGATTCGGGTGTCCTGCTGG 582
Db 645 CGCGTGAAGTGTACGCGTGGGTCCTGGGGAACATGGCGACTCCAGTGTGCTGTGG 704
Qy 583 TCTCTTACCAATCGACGGCATGAAGCTCGGGATTACTGCGAAAAAGCCACACATA 642
Db 705 AGTGGTGAATGTTGGCGGCTTCCCTGAGTCTCTTAACCCAGAACTGGGCACTGAC 764
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Db 825 ATCAAGTGAAAGGTTACACATCTCGGGCCATTG 858
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LOCUS
DEFINITION
603167455F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5255629 5',
mRNA sequence.
BI905403
ACCESSION
BI905403.1 GI:16167906
VERSION
EST.
KEYWORDS
house mouse.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 891)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1645 row: n column: 14
High quality sequence start: 4
High quality sequence stop: 848.
FEATURES
Location/Qualifiers
1. 891
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5255629"
/clone_lib="NCI CGAP Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5].
TGTTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 218 a 221 c 250 g 201 t
ORIGIN
Query Match 13.5%; Score 131.4; DB 13; Length 891;
Best Local Similarity 50.7%; Pred. No. 1.7e-27;
Matches 349; Conservative 0; Mismatches 331; Indels 9; Gaps 1;
Qy 52 AAAGTTGTTGGTGGAGTGGGAAGTGGTGGTCTGCCACAGGTATACGTGCTTCTC 111
Db 136 AAGATTACAGTTGTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 195
Qy 112 AGCGGATCGTTTCCGAGATTGCTTATCGACGTGAACAAAGACAAAGCAGAGGTGAA 171
Db 196 AAGGACTTGGCGGATGAGCTTGGCTTGTGAGTCATGGAAGACAACTCAAGGGCGAG 255
Qy 172 AGCATGACTTAACACGACGACCTTCAAAATACAAAGTCTCGAGGGGTGATATCCT 231
Db 256 ATGATGATCTCCAGCATGCGAGCTCTTCTTTAAACACCAAAATTTGCTCAGCAAA 315
Qy 232 GACTGCGTGGCGGGCCA-----TTGTTATTGTCACATGTGCGATTAAACAAAAA 282
Db 316 GACTACTGTGTAATCGGAACTCCAAGTGGTCAATATACCGGGGGGGCCGCTCAGCAA 375
Qy 283 AATGGACAAACAGGATGGATCTTGTGCAAAAAATGCCAACATTATGCTGGAATCATC 342
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Db      376 GAGGGGAGAGCGGGCTCAACCTGGTCCAGCGAAGCGTGAACATCTTCAAGTTTCATCAT 435
Qy      343 CCCAATGTTCCCAATATGCTCTGATACCATCTGCTTATTCGCACGAATCTCTGTCGAT 402
Db      436 CCCAACATGTCAGTACAGTCCACACTGCAAGCTGCTGATCTCTCCAATCCAGTGGAT 495
Qy      403 GTTTTGACCTATATTAGCTATAGGCGTCAGGGTTTCACATAGCAGAGATTATCGGCTCA 462
Db      496 ATCTTGACCTACGCTGGCTTGGAATAATCAGTGGCTTTCCCAAAAACCGAGTAAATGGAAGT 555
Qy      463 GGTACAGTCTGATACCTGCTGTTTAAATATACATCTCGGAGAGCACTTCAGAGTCTCA 522
Db      556 GGTTCGATCTGATTCAGCGCGGTTCCGTTACTGATGGAGAGAGCGCTGGGGGTTTAC 615
Qy      523 TCGGACAGCATCGATGCTGTGTAATTGGAACATCGTGTATTCGGGTGCTGCTGCTGG 582
Db      616 GCCTGAGCTGTCAAGCTGGTCTCGGAGACATCGGCACTCCAGTGTGCTGTGTTGG 675
Qy      583 TCTTTACCAACTCGACGCGATGAAGTCTCGGATTTACTGCGAAAAGCCAAACCATATA 642
Db      676 AGTGGTGTGAATGTTGCGGCGTCTCCCTGAAGTCTCTTAACCCAGAACTGGGCACTGAC 735
Qy      643 TTTGATCAGATGGTTCATAGATCTTTGAGCAACGCGAGACGCTGCTTACGATATC 702
Db      736 GCAGACAAGGAGCAGTGGAGGAGTTTCAACAGCAGGTGGTGACAGTGCCTACGAGGTG 795
Qy      703 ATCAAGCGCAAGGCTATATCTTCATATGG 731
Db      796 ATCAAGCTGAAGGTTACATCTCTGGG 824

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RESULT 9

AU090981 1097 bp mRNA linear EST 23-JAN-2001
 LOCUS AU090981 lambda ZAP11-Con A stimulated leukocytes Paralicthys
 DEFINITION olivaceus cDNA clone JFConA516f forward similar to Sphyræna
 idiaates Lactate dehydrogenase-A (U80001), mRNA sequence.

ACCESSION AU090981
 VERSION AU090981.1 GI:12391021

SOURCE EST.
 ORGANISM Paralicthys olivaceus

bastard halibut.
 Paralicthys olivaceus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;
 Pleuronectoides; Paralicthysidae; Paralicthys.
 1 (bases 1 to 1097)

REFERENCE Nam, B., Hirono, I. and Aoki, T.
 AUTHORS Identification of expressed genes from Japanese flounder
 TITLE (Paralicthys olivaceus) leukocytes stimulated with Con A/PMA
 JOURNAL Unpublished (2000)

COMMENT Contact: Ikuo Hirono
 Laboratory of Genetics and Biochemistry
 Tokyo University of Fisheries
 Konan 4-5-7, Minato-ku, Tokyo 108, Japan
 Email: hirono@okyo-u-fish.ac.jp.

FEATURES 1..1097
 source /organism="Paralicthys olivaceus"
 /db_xref="taxon:8255"
 /clone="JFConA516f"
 /clone_lib="lambda ZAP11-Con A stimulated leukocytes"
 /cell_type="leukocytes"
 /dev_stage="adult"
 /notes="common name:japanese flounder ; injected with
 peptidoglycan"

BASE COUNT 259 a 293 c 324 g 221 t

ORIGIN

Query Match 13.5%; Score 131.4; DB 9; Length 1097;
 Best Local Similarity 49.5%; Pred. No. 1.9e-27;
 Matches 373; Conservative 0; Mismatches 371; Indels 9; Gaps 1;

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Qy      35 CTGATGCCAAAACAGTAAAGTTGTGTAGTGGAGTGGGAAAGTTGGTCTGCGCACAG 94
Db      121 CTGTTGGCAGCAAGAACAAAGTCCACAGTGTGGCGGTGGCATGTGGCGATCGCCTCG 180
Qy      95 CGTATAGTTGTTCTTCAGGGGATCGTTTCOGAGATTGCTCTTATTCGACGTGAACAAG 154
Db      181 CCATGAGCGTCTCTGCTGAAGGACTTGTGTGATGAGCTGGCCCTGGTTGATGTGATGAGG 240
Qy      155 ACAAGCAGAGGGTGAAGCATGGACTTAAACCCAGCAGCACCTTCAAATAFACAAGGTCTC 214
Db      241 ACAGCTGAAGGTGAGGCCATGGACCTGCAGCAGCGGCTCCCTCTTCTCTCAAGCGCACA 300
Qy      215 GAGCGGTTGATTATCTCTGACTCGCTGGCGCGGCCA-----TTGTTATTGTCACAT 265
Db      301 AGATTGTGCGCAGCAAAAGACTACAGCGTGCACAGCCAACTCCAAGGTGGTAGTGGTACTG 360
Qy      266 GTGGGATTAAACNAAAAATGGAACAACAAGAGTGGATCTTGTCTGCAAAAAATGCCACA 325
Db      361 CCGGCGCCCGCCAGCAGAGGCGGAGCGCTCTCAACCTGTGTCAGCGTAACGTCAACA 420
Qy      326 TTATGCTGAAATCATCCCAATGTTGCCAAATATGCTCTGATACCATCTCTCTTATTG 385
Db      421 TTTTCAAGTTCAATCCCCAATTTGCAAGTACAGCCCAACTGCACTCTGATGGTGG 480
Qy      386 CCACGAATCTGTGCTGATGTTTGAACCTATATTAGCTTATAAGCGCTCAGGGTTTCCACTAA 445
Db      481 TCTCCAACCCAGTGGACATCTTGACCTACGTGGCCTGGAAGCTGAGCGGCTTCCCGGTC 540
Qy      446 GCAGATTATCGGCTCAGGTACAGTTCTGGATACCTGCTGTTTAAATACATCTCGGAG 505
Db      541 ACCGCTCATTTGGCTCTGGCACCAACCTGGGACTCTGCCGCTTTCCGCCACCTCATGGAG 600
Qy      506 AGCACTTCAAGATCTCATCGCAGCATCGATGCTGCTGTGTAATTGAGAACATGGTGATT 565
Db      601 AGAAGCTCCACATCCACCTTCCTCAGCTGTCTGCTGGTATCATCGGAGACACGGAGACT 660
Qy      566 CGGCTGTGCTGTCTGCTCTTACCACATCGACGGCATGAAGCTCCGGGATTTACTGCG 625
Db      661 CCAGTGTGCGCGTGTGGAGCGCGTGAATGTTGCGCGAGTTTCTCTGCAAGGTCTGAACC 720
Qy      626 AAAAAACCAACACATATTTGATCAGATGCGTTTCCATAGATCTTTGAGCAACCGGAG 685
Db      721 CAAAAATGGGAGCTGAGGGGTGACAGCAGAGACTGGAAGCAGGTTTCAAGATGGTGGTTG 780
Qy      686 AGCTGCTTACGATATCATCAAGCGCAAGGCTATATCTTATCATATGGAATCGCAGCGGAT 745
Db      781 ACGAGCCTATGAGGTTCATCAAGCTGAAGGGGTACACTTCTCTGGGCCATTTGGCATGTCTG 840
Qy      746 TACTTCGCATAGTAAAGCGGATTTTAGAGGATA 778
Db      841 TGGCTGACCTGGTGAAGCAATCTTGAAGAACA 873

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RESULT 10

BQ895574

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ895574 951 bp mRNA linear EST 16-AUG-2002

AGENCOURT 8748093 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6335313

5', mRNA sequence.

BQ895574

VERSION BQ895574.1 GI:22287588

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 951)

NIH-MGC http://mgi.nci.nih.gov/

Unpublished (1999)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,

```

Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13797 row: i column: 10
High quality sequence stop: 611.
Location/Qualifiers
1. .951
/organism="Mus musculus"
/db xref="taxon:10090"
/clone="IMAGE:6335313"
/lab host="DH10B (phage-resistant)"
/note="Organ: oocytes; Vector: pCMV-SPORT6.1.ccd;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
NIH MGC Library."
BASE COUNT      234 a 227 c 265 g 222 t 3 others
ORIGIN
Query Match      13.5%; Score 130.8; DB 14; Length 951;
Best Local Similarity 50.7%; Pred. No. 2.7e-27;
Matches 346; Conservative 0; Mismatches 328; Indels 9; Gaps 1;

Qy 52 AAGTTGTTGGTAGTGGGAGTGGGAAGTGTGGGTCTGCCACAGGTATAGTGTCTTC 111
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 99 AAGATTACAGTTGTGGGTGGTGGCTGTGGCATGCTGTGCCATCAGTACTTAATG 158
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 112 AGCGGATCGTTCCGAGATTGCTTATCGACGTGAACAAAGCAAGCAGAGGGTGA 171
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 159 AAGGACTTGGCGGATGAGTTCGCTTGTGACGTCTATGGAAGCAAACTCAAGG 218
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 AGCATGACTTAAACACGAGCAGCCTTCAATACAAAGTCTCGAGCGGTGATTATC 231
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 219 ATGATGATCTCCAGCATGGCAGCTCTTCTTAAACACCAAAATTTGCTCCAGCA 278
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 232 GACTCGCGTGGCGGGCA-----TTGTTATTGTCACTATGTTGGATTAACCAAA 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 279 GACTACTGTGTAACTGCGAACTCCAAAGCTGCTATTATCACCGGGGGCGGTCAG 338
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 283 AATGCAACAACAGATGATGCTTGTGCAAAAATGCCACATATGCTGGAATCATC 342
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 339 GAGGGGAGAGCCGGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTCA 398
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 343 CCCAATGTTGCCAATATGCTTCGTATACCATCTGCTTATTGGCAGCAATCTCTG 402
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 399 CCCAATGTTGCCAATATGCTTCGTATACCATCTGCTTATTGGCAGCAATCTCTG 458
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 403 GTTTTGACCTATATAGCTATAAGCGGTCAAGGTTTCCACTAAGCAGAGTTATCGG 462
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 459 ATCTTGACCTACGTGGCTTGGAAATCAGTGGCTTCCCAAAACCGAGTAATTTGA 518
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 463 GGTACAGTTCTGGATCTGCTCGTTTAAATACATCTCGAGAGCACTTCAAGATCT 522
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 519 GGTGCAATCTGSAATCAGCGCGTTCGGTTACCTGATGGAGAGAGGCTGGGGTT 578
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Qy 523 TCGGACAGCATCGATGCTGTGTAATTGGAAACATGTTGATTCGGGTGTCCTGTGG 582
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 639 AGTGTGTGAATTTGCGCGGTCTCCCTGAAGTCTCTTAAACCCAGAACTGGGCAC 698
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 643 TTTGATCAGATGGTTCATAGATCTTTGAGCAACCGAGAGCGTGTTCAGATATC 702
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 699 GCAGACAGGAGCAGTGGGAGGATTCACAAAGCAGGTGGTGGACAGTGCCTACG 758
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 703 ATCAAGCGAAAGGCTATCTTC 725

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Db 759 ATNCAGCTGAAGGTTACACATC 781
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RESULT 11
BO884746 903 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT_8751063 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6333603
DEFINITION 5', mRNA sequence.
ACCESSION BO884746
VERSION BO884746.1 GI:22276764
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 903)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13793 row: b column: 04
High quality sequence stop: 635.
Location/Qualifiers
1. .903
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/db xref="taxon:10090"
/clone="IMAGE:6333603"
/lab lib="NIH MGC 130"
/lab host="DH10B (phage-resistant)"
/note="Organ: oocytes; Vector: pCMV-SPORT6.1.ccd;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
NIH MGC Library."
BASE COUNT      224 a 219 c 253 g 205 t 2 others
ORIGIN
Query Match      13.4%; Score 130.6; DB 14; Length 903;
Best Local Similarity 50.4%; Pred. No. 3e-27;
Matches 350; Conservative 0; Mismatches 335; Indels 9; Gaps 1;

Qy 52 AAGTTGTTGGTAGTGGGAGTGGGAAGTGTGGGTCTGCCACAGGTATAGTGTCTTC 111
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 112 AGCGGATCGTTTCCGAGATTGCTTATCGACGTGAACAAAGCAAGCAGAGGGTGA 171
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 177 AAGACTTGGCGATGAGCTTGGCCCTTGTGAGCTATGGAAGCAAACTCAAGGGCG 236
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 172 AGCATGACTTAAACACGAGCAGCCTTCAAATACAAAGTCTCGAGCGGTGATTATCT 231
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 237 ATGATGATCTCCAGCATGCGACCTCTTCTTAAACACCAAAATTTGCTCCAGCAA 296
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 232 GACTCGGTGGCGGGCA-----TTGTTATTGTACATGTGGGATTAACCAAAA 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 297 GACTACTGTGTAATCTCGAACTCCAAAGCTGGTCTATTATCACCGGGGGCGGTCAG 356
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 283 AATGGCAACAACAGGATGATCTTGTGCAAAAATGCCAATATGCTGGAATCATC 342
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Qy 357 GAGGGGAGAGCGGCTCAACCTGCTCCAGCGAAAGTGAACATCTTCAAGTTCA 416
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Qy 343 CCCAATGTTGCCAATATGCTTCTCTGATACCATCTGTTATGCCAGGATCTGTGAT 402
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Db 417 CCCAACATTGTCAGTACAGTCCACACTGCAAGCTGCTGATGCTCTCCAAATCCAGTGGAT 476
 QY 403 GTTTTGACCTATATTAGCTATAAGGGCTCAGGGTTTCCACTAAGCAGAGAGTTATCGGCTCA 462
 Db 477 ATCTTGACCTACGTGGCTTGGAATATCAGTGGCTTTCCCAAAACCGAGTAATGGAGT 536
 QY 463 GGTACAGTTCGTGATACCTGCTGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCA 522
 Db 537 GGTGCAATCTGGAATTCAGCGCGGTTCCTGTTACCTGATGAGAGAGGCTGGGGGTTTCA 596
 QY 523 TCGGACAGATCGATGCTGTGTAATTTGGAGACATGGTATTCGGGTGCTGCTGCTGG 582
 Db 597 GCCTGAGCTGTACGCTGGCTTCTGNGAGAACATGCGACTCCAGTGTGCTGTGTTGG 656
 QY 583 TCTTCTACCAACATCGACGCGCTCAAGCTCCGGGATTTACTGCGAAAGACCAACCATCA 642
 Db 657 AGTGGTGTGAATGTGCGCGCTCTCCCTGAAGTCTCTTAACCCAGAACTGGGCACTGAC 716
 QY 643 TTTGATCAGATCGGTTCCATAGAACTTTGAGCAAAACGGGACAGCGTGTTCAGATATC 702
 Db 717 GCAGACAAGGAGCAGTGGAGGAGGTTTCAACAGCAGGTGGTGACAGTGCCTACGAAGTG 776
 QY 703 ATCAAGCGCAAGCTATATCTTCATATGGAATCG 736
 Db 777 ATCAAGCTGAAGGTTACATCTCGGCGCATTTG 810

RESULT 12
 BO886472
 LOCUS
 DEFINITION BO886472 959 bp mRNA linear EST 16-AUG-2002
 5', mRNA sequence.
 BO886472
 VERSION BO886472.1 GI:22278486
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 959)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
 Ph.D.
 CDNA Library Preparation: ResGen, Invitrogen Corp
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL3784 row: 1 column: 16
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 1. 959
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 /lab_host="DH10B (phage-resistant)"
 /notes="Organ: oocytes; Vector: pCMV-SPORT6.1.ccdB;
 Site 1: EcorV; Site 2: NotI; Cloned unidirectionally.
 Primer: Oligo dT. Average insert size 1.95 kb.
 Constructed by ResGen, Invitrogen Corp. Note: this is a
 NIH MGC library."

BASE COUNT 233 a 231 c 268 g 226 t 1 others
 ORIGIN
 Query Match 13.4%; Score 130; DB 14; Length 959;
 Best Local Similarity 50.4%; Pred. No. 4.6e-27;
 Matches 350; Conservative 0; Mismatches 335; Indels 9; Gaps 1;

QY 52 AAAGTTGTGTAGTGGAGTGGAAAGTGTGGGTCTGCCACAGCGGTATACGTTGCTTCTC 111
 Db 74 AAGATTACAGTTGTTGGGGTGGTGGTGTGGCATGGCTTGTGCCATCAGTATCTTAATG 133
 QY 112 AGGGCATCGTTTCCGAGATTGCTTATTCGACGTGAACAAGACAAAGCAGAGGGTGAA 171
 Db 134 AAGGACTTGGCGGATGAGCTTGGCTTGTGACGTGATGAAGACAAACTCAAGGGCGAG 193
 QY 172 AGCATGAGCTTAAACCCACAGCAGCCTTCAAAATACAAAGTCTCGAGCGGTGATTATCCT 231
 Db 194 ATGATGGATCTCCAGATGGGAGCTCTTCTTTAAACACCAAAAATTGTCTCCAGCAA 253
 QY 232 GACTCGCTGGCGCGGCCA-----TTGTTATTGTCCATGTGGGATTAACCAAAA 282
 Db 254 GACTACTGTGTAATGCGAACTCCAAAGCTGGTCAATTATCACCGCGGGGCGGCTCAGCA 313
 QY 283 AATGGCAACAAGAGTGGATCTTGTCTGCAAAAATGCCAATATATGCTGGAATATC 342
 Db 314 GAGGGGAGAGCGGCTCAACCTGGTCCAGCGAAACGTGAACATCTTCAAGTTTCATCT 373
 QY 343 CCCAATGTTGCCAAATATGCTCTGATACCATCTCTTATTGCGACGAATCCTGTCGAT 402
 Db 374 CCACATTTGTCAAGTACAGTCCACTCAAGCTGCTGATGCTCTCAATCCAGTGGAT 433
 QY 403 GTTTTGACCTATATTAGCTATTAAGGCGTCAGGGTTTCCACTAAGCAGAGATTTCGGCTCA 462
 Db 434 ATCTTGACCTACGTGGCTTGGAAATCAGTGGCTTTCCCAAAACCGAGTAATGGAGT 493
 QY 463 GGTACAGTTCTCGATACCTGCTGTTTAAATACATCTCGGAGAGCACTTCAAGATCTCA 522
 Db 494 GGTGCAATCTGGAATTCAGCGGGTTCCTGATGGGAGAGAGGCTGGGGGTTTCA 553
 QY 523 TCGGACAGCATCGATGCTGCTGTAATTGAGAACATGTTGATTCGGGTGCTGCTG 582
 Db 554 GCGTGAGCTGTACGCTGGGTCTCTGGGAGAACATGGGACTTCCAGTGTGCTGTG 613
 QY 583 TCTCTTACCACATCGACGGCATGAAGTCTCCGGGATTTACTGCGAAAGCAACCACTA 642
 Db 614 AGTGGTGTGAATGTTGGCGGCTCTCCCTGAAGTCTCTTAACCCAGAACTGGGCACTGAC 673
 QY 643 TTTGATCAAGATGCGTTTCCATAGATCTTTAGCAAAACCGGAGACGCTGTTACGATATC 702
 Db 674 GCAGACAGGAGCAGTGGAAAGGAGTTTCAACAGCAGGTGGTGACAGTGCCTACGAGGTG 733
 QY 703 ATCAAGCGCAAGGCTATATCTTCATATGGAATCG 736
 Db 734 ATCAAGCTGAAGGTTACACATCTCTGGGCCATTG 767

CNS06YKH 645 bp DNA linear GSS 06-JUL-2001
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 of Kluyveromyces thermotolerans, genomic survey sequence.
 AL421143
 VERSION AL421143.1 GI:12204342
 GSS.
 Kluyveromyces thermotolerans.
 Kluyveromyces thermotolerans
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 1 (bases 1 to 645)
 Souciot, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
 Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
 de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
 Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
 Saurin, W., Tekai, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
 Wincker, P. and Weissenbach, J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 FEBS Lett. 487 (1), 3-12 (2000)
 20584711

RESULT 13
 CNS06YKH/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE

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208	Db	GACTACTGTGTAACTGCGGAACTCCAAGCTGGTCATTTATCACCGCGGGGCCGTGAGCAA	267
283	Qy	AATGCACAAAACAGGATGGGATCTTGTCGCAAAAAATGCCAACAATTATGCTGGAATCATC	342
268	Db	GAGGGGAGAGCCCGGCTCAACCTGGTCCAGCGAAGCGTGAACATCTTCAAGTTTCATCAT	327
343	Qy	CCCAATGTTGCCAAATATGCTCTCTGATACCATCCTCTCTTATTGCCACGAATCCTGTCCGAT	402
328	Db	CCCAACATTTGTCAGTACAGTCCACACTGCAAGCTGCTGNTCGTCTCCAATCCAGTGGAT	387
403	Qy	GTTTTGACCTATATTAAGCTATAGGCGGTCAAGGTTTCCACTAAGCAGAGATTATCGGCTCA	462
388	Db	ATCTTGACCTACGTGGCTTGGAATAATCAGTGGGCTTTCCCAAAAACCGAGTAATTGGAACT	447
463	Qy	GGTACAGTTCTGGATATCTGCTCGTTTTAAATATACATCCTCGGAGAGCACTTCAAGATCTCA	522
448	Db	GGTTTGCATCTGGATTTCAGCGCGGGTTCCGGTTACTCTGATGGGAGAGAGGCTGGGGGTT	507
523	Qy	TCGGACAGCATCGATGCTGTGTAAATTGGAGAACATGGTGATTTCGGGTGTCCTCTCTGG	582
508	Db	CGCTGAGCTGTACGGCTGGGCTCGGGAGAACATGGCGACTCCCAAGTGTGCTGTGTGG	567
583	Qy	TCTCTTACCAACATCGACGCATGAAGCTCCGGGATTTACTGCGAAAGACCAACACACATA	642
568	Db	AGTGGTGTGAATGTTGCGCGGCTCTCCCTGAAGTCTCTTAAACCAGACTGGGGCACTGAC	627
643	Qy	TTTGATCAGAATCGGTTCCATAGAATCTTTGAGCAAAACCGGAGACGCTGCTTTACGATATC	702
628	Db	GCAGACAAGGAGCAGTGGAGGGAGTTCAACAGCAGGTGTGGACAGTGCCTACAGGTG	687
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/clone_lib="NCI_CGAP_Mam6"
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/dev stage="5 months"
/lab host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
231 a 214 c 267 g 212 t

BASE COUNT
ORIGIN

Query Match 13.3%; Score 129.6; DB 13; Length 924;
Best Local Similarity 50.4%; Pred. No. 6e-27;
Matches 349; Conservative 0; Mismatches 334; Indels 9; Gaps 1;

OY 52 AAAGTTGTGGTGTGGAGTGGGAGGTGTGGGTCTGCCACAGCPATACGTTGCTTCTC 111
|||
28 AAGATTACAGTTGTTGGGGTGTGGTGTGTTGGCATGCTTGTGCCATCAGTATCTTAATG 87
|||

112 AGCGSCATCGTTTCCGAGATTGTCTTATCGAGCTGAACAAAGACAAACAGCAGGGTCAA 171
|||
88 AAGGACTTGGCGGATAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 147
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172 AGCATGGACCTTAAACACAGCGACGACCTTCAAATACAAAGGTCTCGAGCGGGTCAATTATCCT 231
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